

Wed Nov 13 14:22:40 2002

us-09-676-436-3.limit.rge

Page 1

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 05:35:40 ; Search time 8243 Seconds

(without alignments)  
17617.736 Million cell updates/sec

Title: US-09-676-436-3

Perfect score: 4990  
Sequence: 1 ctgaagactctccgatga.....ggtattataggaagctc 4990

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 993650

Minimum DB seq length: 8

Maximum DB seq length: 100

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 1000 summaries

Database :

1: GenEmbl:\*  
2: gb\_ba:\*  
3: gb\_htg:\*  
4: gb\_in:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_yi:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rnd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	29.6	0.6	87	3	DDIDDKD	M59747 D. discoiden
2	26	0.5	100	6	AR007403	AR007403 Sequence
3	25.8	0.5	81	6	AX381834	AX381834 Sequence
4	25.4	0.5	96	5	AF025984	AF025984 Paratichit
5	25.2	0.5	65	6	AX486379	AX486379 Sequence
6	25.2	0.5	70	1	AX033167	AX033167 Sequence
7	25.2	0.5	70	6	AX033159	AX033159 Sequence
8	25.2	0.5	83	4	RABPFKM18	165769 Sequence 5
9	24.8	0.5	92	6	AX173377	M14473 Rabbit musc
10	24.8	0.5	71	6	AX173377	AX173377 Sequence
11	24.6	0.5	71	6	AR140801	AR140801 Sequence
12	24.6	0.5	71	6	I93480	I93480 Sequence 78
13	24.6	0.5	71	6	I93480	I93480 Sequence 78
14	24.6	0.5	73	3	AR203036	AR203036 Sequence
15	24.4	0.5	98	6	AR203036	AR203036 Sequence
16	24.4	0.5	98	6	AR203036	AR203036 Sequence
17	24.4	0.5	100	3	DROTRANSIN	AR007408 Sequence
18	24.2	0.5	65	6	AX486377	AX486377 Sequence
19	24	0.5	51	10	U921771	U92173 Mus musculu
20	24	0.5	65	6	AX48371	AX48371 Sequence
21	24	0.5	65	6	AX207310	AX207310 Sequence
22	24	0.5	88	6	AB04840511	AB048411 Homo sapi
23	24	0.5	97	6	AR014621	AR014621 Sequence
24	24	0.5	97	6	BD010413	BD010413 Chimeric
25	24	0.5	97	6	I26754	I26754 Sequence 54
26	24	0.5	82	4	AF294354S5	AF294358 Bos tauru
27	23.8	0.5	87	14	AF050514	AF050514 Human end
28	23.8	0.5	90	3	TRBANTATC2	M28495 Trypanosoma
29	23.8	0.5	91	10	MM0130784	A0130784 Mus muscu
30	23.8	0.5	94	6	AX326634	AX326634 Sequence
31	23.8	0.5	94	6	AX326671	AX326671 Sequence
32	23.8	0.5	94	9	S52152519	S52191 CD11b-Leuko
33	23.8	0.5	96	5	AF025985	AF025985 Paratichit
34	23.6	0.5	78	9	HS4305430	AJ305430 Homo sapi
35	23.6	0.5	87	6	AR062856	AR062856 Sequence
36	23.6	0.5	88	11	HUM07770A	L31186 Human STR U
37	23.6	0.5	98	6	AX326603	AX326603 Sequence
38	23.6	0.5	99	6	AX059602	AX059602 Sequence
39	23.6	0.5	100	5	AP025983	AF025983 Paratichit
40	23.4	0.5	77	6	A20465	A20465 oligonucleo
41	23.4	0.5	79	10	AXAP1YC	M32437 Rat/polyoma
42	23.4	0.5	80	9	AR480570	AF480570 Homo sapi
43	23.4	0.5	83	6	AX240922	AX240922 Sequence
44	23.4	0.5	89	6	S72771	S72771 Immunoglobu
45	23.4	0.5	99	11	HSPE99C03	AX015186 Sequence
46	23.2	0.5	65	6	AX483262	AX483262 Sequence
47	23.2	0.5	87	5	CHRMILAS	M19461 Chicken c-m
48	23.2	0.5	97	4	OC072578	U72578 Oryctolagus
49	23.2	0.5	100	5	AF174523	AF174523 Bufo dana
50	23.2	0.5	89	17	HSEXR35	T10934 H.sapiens D
51	23	0.5	90	6	AX391840	AX391840 Sequence
52	23	0.5	91	9	HSU32336	U32336 Human pre-B
53	23	0.5	94	6	AR170294	AR170294 Sequence
54	23	0.5	94	6	AX007122	AX007122 Sequence
55	23	0.5	94	6	AX020432	AX020432 Sequence
56	23	0.5	94	6	E51068	E51068 Novel Bsch
57	23	0.5	98	14	AF292795	AF292795 HIV-1 cto
58	23	0.5	100	9	HS43B7E	Z58533 H.sapiens C
59	23	0.5	100	9	HS43B7E	Z58534 H.sapiens C
60	22.8	0.5	55	9	HSADDS24	AF000104 Homo sapi
61	22.8	0.5	55	10	S69914	S69914 BCL-2-RNA P
62	22.8	0.5	65	6	AX484094	AX484094 Sequence
63	22.8	0.5	76	6	A20466	A20466 oligonucleo
64	22.8	0.5	76	6	AR007324	AR007324 Sequence
65	22.8	0.5	76	6	AR007324	AR007324 Sequence

C 66	22.8	0.5	85	11	ALB07913	C 139	21.8	0.4	65	14	SVANKV3
C 67	22.8	0.5	90	9	HSREPAL3	C 140	21.8	0.4	66	9	HUMTCDC
C 68	22.8	0.5	94	3	BYU52988	C 141	21.8	0.4	73	6	AI9086
C 69	22.8	0.5	94	6	AX088804	C 142	21.8	0.4	73	9	AF147985
C 70	22.8	0.5	95	6	E03691	C 143	21.8	0.4	74	6	AI9085
C 71	22.8	0.5	96	6	AR107453	C 144	21.8	0.4	77	5	AX381381
C 72	22.8	0.5	96	10	MUSIGHNF	C 145	21.8	0.4	77	6	AF517937
C 73	22.8	0.5	100	11	HUMUT1990A	C 146	21.8	0.4	79	5	AF517937
C 74	22.6	0.5	51	6	AX161521	C 147	21.8	0.4	79	6	AR145885
C 75	22.6	0.5	51	6	AX161523	C 148	21.8	0.4	80	6	AX030305
C 76	22.6	0.5	51	6	AX199647	C 149	21.8	0.4	81	6	AR110371
C 77	22.6	0.5	64	6	AX381699	C 150	21.8	0.4	81	6	BD009391
C 78	22.6	0.5	69	9	AF189373	C 151	21.8	0.4	83	6	AI9093
C 79	22.6	0.5	69	9	APU09225	C 152	21.8	0.4	83	6	AI9095
C 80	22.6	0.5	84	10	MUSIGHNF	C 153	21.8	0.4	83	6	AX146299
C 81	22.6	0.5	87	14	AF050512	C 154	21.8	0.4	85	14	SVANKM1
C 82	22.6	0.5	93	9	HUMTLV124	C 155	21.8	0.4	86	6	AI9096
C 83	22.6	0.5	94	10	RATOTCA07	C 156	21.8	0.4	87	6	AI9094
C 84	22.6	0.5	100	6	AX379183	C 157	21.8	0.4	94	10	MMVIMV73
C 85	22.6	0.5	81	14	AF2272172	C 158	21.8	0.4	95	6	A33974
C 86	22.4	0.4	81	14	AF2272172	C 159	21.8	0.4	95	6	A33975
C 87	22.4	0.4	90	9	CORINSORFB	C 160	21.8	0.4	96	6	AX039308
C 88	22.4	0.4	90	9	AF5371	C 161	21.8	0.4	98	6	AX039308
C 89	22.4	0.4	95	6	AR061176	C 162	21.8	0.4	98	6	AX039308
C 90	22.4	0.4	95	6	AR061176	C 163	21.8	0.4	99	6	AX341452
C 91	22.4	0.4	95	6	HSW62H113	C 164	21.8	0.4	100	6	AX039309
C 92	22.4	0.4	96	9	AB044117	C 165	21.8	0.4	100	6	AX039309
C 93	22.4	0.4	97	6	AR014618	C 166	21.8	0.4	100	6	AX039309
C 94	22.4	0.4	97	6	BD010410	C 167	21.8	0.4	100	6	AX039309
C 95	22.4	0.4	97	6	BD010410	C 168	21.8	0.4	100	6	AX039309
C 96	22.4	0.4	98	9	HUMMCR03	C 169	21.8	0.4	100	6	AX039309
C 97	22.4	0.4	51	6	AX162466	C 170	21.8	0.4	100	6	AX039309
C 98	22.4	0.4	51	6	AX162466	C 171	21.8	0.4	100	6	AX039309
C 99	22.4	0.4	51	6	AX162466	C 172	21.8	0.4	100	6	AX039309
C 100	22.2	0.4	65	6	AX165549	C 173	21.8	0.4	100	6	AX039309
C 101	22.2	0.4	68	9	S81023	C 174	21.8	0.4	100	6	AX039309
C 102	22.2	0.4	71	6	AR058866	C 175	21.8	0.4	100	6	AX039309
C 103	22.2	0.4	71	6	AR058866	C 176	21.8	0.4	100	6	AX039309
C 104	22.2	0.4	71	6	AR058866	C 177	21.8	0.4	100	6	AX039309
C 105	22.2	0.4	73	8	AR140982	C 178	21.8	0.4	100	6	AX039309
C 106	22.2	0.4	76	6	AX080171	C 179	21.8	0.4	100	6	AX039309
C 107	22.2	0.4	82	3	AF323690	C 180	21.8	0.4	100	6	AX039309
C 108	22.2	0.4	85	6	AR054868	C 181	21.8	0.4	100	6	AX039309
C 109	22.2	0.4	85	6	AR054868	C 182	21.8	0.4	100	6	AX039309
C 110	22.2	0.4	87	6	AR211441	C 183	21.8	0.4	100	6	AX039309
C 111	22.2	0.4	87	6	AR211441	C 184	21.8	0.4	100	6	AX039309
C 112	22.2	0.4	90	9	S82667	C 185	21.8	0.4	100	6	AX039309
C 113	22.2	0.4	90	9	S82667	C 186	21.8	0.4	100	6	AX039309
C 114	22.2	0.4	92	10	MMU03545	C 187	21.8	0.4	100	6	AX039309
C 115	22.2	0.4	94	6	AX134535	C 188	21.8	0.4	100	6	AX039309
C 116	22.2	0.4	94	6	AX134535	C 189	21.8	0.4	100	6	AX039309
C 117	22.2	0.4	94	6	AX134535	C 190	21.8	0.4	100	6	AX039309
C 118	22.2	0.4	94	6	AX134535	C 191	21.8	0.4	100	6	AX039309
C 119	22.2	0.4	100	6	AX020439	C 192	21.8	0.4	100	6	AX039309
C 120	22.2	0.4	40	9	AB076378	C 193	21.8	0.4	100	6	AX039309
C 121	22.2	0.4	65	6	AX486026	C 194	21.8	0.4	100	6	AX039309
C 122	22.2	0.4	65	6	AX486026	C 195	21.8	0.4	100	6	AX039309
C 123	22.2	0.4	73	6	AX080404	C 196	21.8	0.4	100	6	AX039309
C 124	22.2	0.4	78	10	MUSICAVB	C 197	21.8	0.4	100	6	AX039309
C 125	22.2	0.4	81	6	AF5654	C 198	21.8	0.4	100	6	AX039309
C 126	22.2	0.4	91	8	YSCMP041	C 199	21.8	0.4	100	6	AX039309
C 127	22.2	0.4	92	6	AX388866	C 200	21.8	0.4	100	6	AX039309
C 128	22.2	0.4	93	10	CRUGP102	C 201	21.8	0.4	100	6	AX039309
C 129	22.2	0.4	94	8	YSCGNCX2	C 202	21.8	0.4	100	6	AX039309
C 130	22.2	0.4	95	11	HSPELAE07	C 203	21.8	0.4	100	6	AX039309
C 131	22.2	0.4	95	11	HSPELAE07	C 204	21.8	0.4	100	6	AX039309
C 132	22.2	0.4	96	10	MUSIGCHF	C 205	21.8	0.4	100	6	AX039309
C 133	22.2	0.4	98	6	AX326604	C 206	21.8	0.4	100	6	AX039309
C 134	22.2	0.4	98	6	AX326604	C 207	21.8	0.4	100	6	AX039309
C 135	22.2	0.4	98	6	AX326604	C 208	21.8	0.4	100	6	AX039309
C 136	21.8	0.4	100	9	HSPE75F09	C 209	21.8	0.4	100	6	AX039309
C 137	21.8	0.4	54	6	HUMPTHEP1	C 210	21.8	0.4	100	6	AX039309
C 138	21.8	0.4	56	9	AR039666	C 211	21.8	0.4	100	6	AX039309
C 139	21.8	0.4	64	11	HUMNTOCPO2						
C 140	21.8	0.4	64	11	HUMNTOCPO2						
C 141	21.8	0.4	64	11	HUMNTOCPO2						
C 142	21.8	0.4	64	11	HUMNTOCPO2						
C 143	21.8	0.4	64	11	HUMNTOCPO2						
C 144	21.8	0.4	64	11	HUMNTOCPO2						
C 145	21.8	0.4	64	11	HUMNTOCPO2						
C 146	21.8	0.4	64	11	HUMNTOCPO2						
C 147	21.8	0.4	64	11	HUMNTOCPO2						
C 148	21.8	0.4	64	11	HUMNTOCPO2						
C 149	21.8	0.4	64	11	HUMNTOCPO2						
C 150	21.8	0.4	64	11	HUMNTOCPO2						
C 151	21.8	0.4	64	11	HUMNTOCPO2						
C 152	21.8	0.4	64	11	HUMNTOCPO2						
C 153	21.8	0.4	64	11	HUMNTOCPO2						
C 154	21.8	0.4	64	11	HUMNTOCPO2						
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C 164	21.8	0.4	64	11	HUMNTOCPO2						
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C 180	21.8	0.4	64	11	HUMNTOCPO2						
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C 193	21.8	0.4	64	11	HUMNTOCPO2						
C 194	21.8	0.4	64	11	HUM						

212	21.4	0.4	81	14	AF018313	AF018313 Hepatitis	285	21	0.4	50	3	GIACA33	LA9332 SRS of NotI
213	21.4	0.4	84	6	A94799	A94799 Sequence 43	286	21	0.4	51	6	AX117257	AX117257 Sequence
214	21.4	0.4	84	6	A95594	A95594 Sequence 9	287	21	0.4	55	14	HIV1045085	HIV1045085
215	21.4	0.4	84	6	E03577	E03577 DNA sequence	288	21	0.4	60	6	A93058	A93058 Sequence 35
216	21.4	0.4	89	8	AF001054	AF001054 GigaSpora	289	21	0.4	60	6	AR051992	AR051992 Sequence
217	21.4	0.4	90	6	AR170725	AR170725 Sequence	290	21	0.4	60	6	AR060399	AR060399 Sequence
218	21.4	0.4	90	6	AX114637	AX114637 Sequence	291	21	0.4	60	6	AR074851	AR074851 Sequence
219	21.4	0.4	90	6	AX114763	AX114763 Sequence	292	21	0.4	60	6	AR078848	AR078848 Sequence
220	21.4	0.4	90	6	AX118692	AX118692 Sequence	293	21	0.4	60	6	AR128957	AR128957 Sequence
221	21.4	0.4	90	6	AX128109	AX128109 Sequence	294	21	0.4	60	6	E65257	E65257 Mutant of E
222	21.4	0.4	90	6	E12579	E12579 Probe, 4/19	295	21	0.4	62	9	S52152S31	S52152S31
223	21.4	0.4	90	6	E12580	E12580 Probe, 4/19	296	21	0.4	65	6	AX484026	AX484026 Sequence
224	21.4	0.4	90	6	E13639	E13639 Probe, 4/19	297	21	0.4	65	6	AX485310	AX485310 Sequence
225	21.4	0.4	90	6	E17120	E17120 DNA probe.	298	21	0.4	65	6	AX485904	AX485904 Sequence
226	21.4	0.4	90	6	AF317945	AF317945 Arabidops	299	21	0.4	65	6	AX486079	AX486079 Sequence
227	21.4	0.4	92	8	AF420513	AF420513 Salmo sal	300	21	0.4	66	6	AX167457	AX167457 Sequence
228	21.4	0.4	93	6	AR209741	AR209741 Sequence	301	21	0.4	72	9	AF043873	AF043873 Homo sapi
229	21.4	0.4	95	10	HUMCFTR12	M55036 Human cysti	302	21	0.4	73	6	AX233516	AX233516 Sequence
230	21.4	0.4	95	10	MMU403408	AJ403408 M. musculu	303	21	0.4	74	6	AR011572	AR011572 Sequence
231	21.4	0.4	97	6	A74708	A74708 Sequence 39	304	21	0.4	77	8	118210	118210 Sequence 45
232	21.4	0.4	97	6	A77687	A77687 Sequence 39	305	21	0.4	77	8	APH505663	APH505663 Sequence 2
233	21.4	0.4	98	6	I91508	I91508 Sequence 42	306	21	0.4	78	6	103641	103641 Sequence 2
234	21.4	0.4	98	6	HSPHA825	AX13364 Human mRNA	307	21	0.4	78	6	107834	107834 Sequence 2
235	21.2	0.4	43	6	AX484373	AX484373 Sequence	308	21	0.4	80	6	AR77721	AR77721 Sequence 15
236	21.2	0.4	43	6	AX484373	AX484373 Sequence	309	21	0.4	80	6	AR017752	AR017752 Sequence
237	21.2	0.4	51	6	AR134229	AR134229 Sequence	310	21	0.4	80	6	AR094929	AR094929 Sequence
238	21.2	0.4	54	6	AR134229	AR134229 Sequence	311	21	0.4	80	6	AR165588	AR165588 Sequence
239	21.2	0.4	54	6	AR187399	AR187399 Sequence	312	21	0.4	81	9	AY083572	AY083572 Sequence
240	21.2	0.4	59	3	NEMMTEAS	M19848 A. gum mlti	313	21	0.4	81	11	G67356	G67356 3A316FMD G
241	21.2	0.4	64	6	AR160000	AR160000 Sequence	314	21	0.4	82	6	AR038755	AR038755 Sequence
242	21.2	0.4	64	6	AR160001	AR160001 Sequence	315	21	0.4	82	6	AR059641	AR059641 Sequence
243	21.2	0.4	65	6	AX080195	AX080195 Sequence	316	21	0.4	82	6	EC1RRN03	EC1RRN03 Sequence
244	21.2	0.4	65	6	AX483021	AX483021 Sequence	317	21	0.4	82	8	NARARN03	NARARN03 Sequence
245	21.2	0.4	65	6	AX485036	AX485036 Sequence	318	21	0.4	83	6	PYTRRN03	PYTRRN03 Sequence
246	21.2	0.4	67	3	S52308	S52308 dpy-10 (el2	319	21	0.4	83	6	AX361504	AX361504 Sequence
247	21.2	0.4	67	3	S67757	S67757 prostaacycl	320	21	0.4	85	9	AV041942	AV041942 Neclomys
248	21.2	0.4	74	6	AX098134	AX098134 Sequence	321	21	0.4	85	9	HSTR14D	HSTR14D human Chro
249	21.2	0.4	75	6	FA65710S10	FA65710S10 Sequence	322	21	0.4	86	6	AR042760	AR042760 Sequence
250	21.2	0.4	76	6	AX080170	AX080170 Homo sapi	323	21	0.4	86	6	AR081435	AR081435 Sequence
251	21.2	0.4	78	6	CBE345100	AX345100 Carpinus	324	21	0.4	86	6	AR103763	AR103763 Sequence
252	21.2	0.4	80	6	AX172495	AX172495 Sequence	325	21	0.4	88	8	AF001051	AF001051 GigaSpora
253	21.2	0.4	81	6	AR030404	AR030404 Sequence	326	21	0.4	89	6	AX181695	AX181695 Sequence
254	21.2	0.4	81	6	AF312866S1	AF312866 Homo sapi	327	21	0.4	89	8	AF001069	AF001069 GigaSpora
255	21.2	0.4	86	5	AF044757	AF044757 Plynopro	328	21	0.4	90	6	AX089742	AX089742 Sequence
256	21.2	0.4	86	5	AX240909	AX240909 Sequence	329	21	0.4	90	6	AX089743	AX089743 Sequence
257	21.2	0.4	86	5	AF275602	AJ489837 Quercus p	330	21	0.4	90	6	AX090197	AX090197 Sequence
258	21.2	0.4	86	11	AF275602	AF275602 Bos tauru	331	21	0.4	90	6	AX090198	AX090198 Sequence
259	21.2	0.4	87	6	AX033426	AX033426 Sequence	332	21	0.4	90	6	GORINSORA	GORINSORA Gorilla end
260	21.2	0.4	88	8	AB006094	AB006094 Actinidia	333	21	0.4	92	10	AY041796	AY041796 Oryzomys
261	21.2	0.4	88	9	HUMICHTVMA	M87021 Human immun	334	21	0.4	93	9	HOHRTLV13	HOHRTLV13 Sequence
262	21.2	0.4	89	3	OPR81MVA3P	M63171 O. fallax 81	335	21	0.4	93	9	HOHRTLV13	HOHRTLV13 Sequence
263	21.2	0.4	90	1	EVREC33RE	XS5563 P. vulgaris	336	21	0.4	94	6	AX366494	AX366494 Sequence
264	21.2	0.4	90	5	XM082794	XM082794 Xiphophorus	337	21	0.4	96	5	AF459837	AF459837 Gallus ga
265	21.2	0.4	90	5	XM082798	XM082798 Xiphophorus	338	21	0.4	96	5	AF459838	AF459838 Gallus ga
266	21.2	0.4	90	5	XM082801	XM082801 Xiphophorus	339	21	0.4	96	5	AF459839	AF459839 Gallus ga
267	21.2	0.4	90	5	XM082801	XM082801 Xiphophorus	340	21	0.4	96	5	AF517938	AF517938 Labo der
268	21.2	0.4	90	5	SA169552	S38640 Pseudogene	341	21	0.4	96	9	AY006263	AY006263 Homo sapi
269	21.2	0.4	90	9	DDIACCTMIA	U01265 SLIME moid	342	21	0.4	98	6	AX107888	AX107888 Sequence
270	21.2	0.4	95	3	AR026961	AR026961 Sequence	343	21	0.4	99	10	MUSCATINA	M61019 Mouse carbo
271	21.2	0.4	95	6	ATR243379	ATR243379 Arabidops	344	21	0.4	100	6	E01897	E01897 Part of seq
272	21.2	0.4	95	6	AX052995	AX052995 Sequence	345	21	0.4	100	6	109068	109068 Sequence 4
273	21.2	0.4	96	6	AX052995	AX052995 Sequence	346	21	0.4	48	6	AX378186	AX378186 Sequence
274	21.2	0.4	98	6	AX13606	AX13606 Oligonucleo	347	21	0.4	48	6	AX441070	AX441070 Sequence
275	21.2	0.4	98	6	AX468159	AX468159 Sequence	348	21	0.4	48	6	HSU14062	HSU14062 Human T cel
276	21.2	0.4	98	6	E03008	E03008 DNA encodin	349	21	0.4	49	6	AX441075	AX441075 Sequence
277	21.2	0.4	98	10	AF144397	AF144397 Mus muscu	350	21	0.4	50	6	AX199648	AX199648 Sequence
278	21.2	0.4	99	8	AG234786	AG234786 Plumb s	351	21	0.4	54	6	AR042332	AR042332 Sequence
279	21.2	0.4	100	6	AX3851	AX3851 Sequence 25	352	21	0.4	54	6	AX081483	AX081483 Sequence
280	21.2	0.4	100	6	AX3851	AX3851 Sequence 25	353	21	0.4	58	1	AF092845	AF092845 Enterooc
281	21.2	0.4	100	6	AF133138	AF133138 Homo sapi	354	21	0.4	60	8	AX092845	AX092845 Sequence
282	21.2	0.4	100	9	FI93462S18	FI93462S18 Pan trogl	355	21	0.4	60	8	TOHCPR5A	TOHCPR5A Sequence
283	21.2	0.4	100	9	AX424969	AX424969 Sequence	356	21	0.4	63	6	AR106439	AR106439 Sequence
284	21.2	0.4	37	6	AX424969	AX424969 Sequence	357	21	0.4	63	6	AX482945	AX482945 Sequence

C 358	20.8	0.4	65	6	AX484001	AX484001 Sequence	431	20.8	0.4	99	6	A08898	A08898 H. sapiens (
C 359	20.8	0.4	68	6	AX1834	AX1834 Sequence 3	C 432	20.8	0.4	99	6	ARI66875	ARI66875 Sequence
C 360	20.8	0.4	70	6	A35706	A35706 Synthetic o	C 433	20.8	0.4	99	6	AX023619	AX023619 Sequence
C 361	20.8	0.4	70	6	A35709	A35709 Synthetic o	C 434	20.8	0.4	99	6	AX099377	AX099377 Sequence
C 362	20.8	0.4	70	6	ARI68954	ARI68954 Sequence	C 435	20.8	0.4	99	6	AX192501	AX192501 Sequence
C 363	20.8	0.4	70	9	S65093S09	S65103 OTC-Ornithi	C 436	20.8	0.4	99	6	I14841	I14841 Sequence 9
C 364	20.8	0.4	72	6	AX344119	AX344119 Sequence	C 437	20.8	0.4	99	6	I65495	I65495 Sequence 5
C 365	20.8	0.4	72	6	AX344123	AX344123 Sequence	C 438	20.8	0.4	100	5	AF174524	AF174524 Bufo viri
C 366	20.8	0.4	73	6	AX277693	AX277693 Sequence	C 439	20.8	0.4	100	5	AF174525	AF174525 Bufo viri
C 367	20.8	0.4	76	11	AL672133	AL672133 Arabidops	C 440	20.8	0.4	100	5	AF174526	AF174526 Bufo viri
C 368	20.8	0.4	78	9	AF17991	AF17991 Homo sapi	C 441	20.8	0.4	100	6	A76049	A76049 Sequence 33
C 369	20.8	0.4	78	14	AF109765	AF109765 Hepatitis	C 442	20.8	0.4	100	6	AX039309	AX039309 Sequence
C 370	20.8	0.4	80	6	I34338	I34338 Sequence 37	C 443	20.8	0.4	100	6	AX039518	AX039518 Sequence
C 371	20.8	0.4	80	6	AX172504	AX172504 Sequence	C 444	20.8	0.4	100	6	E22365	E22365 Dna encodin
C 372	20.8	0.4	80	6	E03129	E03129 cDNA encodi	C 445	20.6	0.4	51	6	AX162674	AX162674 Sequence
C 373	20.8	0.4	80	9	AF088685	AF088685 Homo sapi	C 446	20.6	0.4	51	6	AX162465	AX162465 Sequence
C 374	20.8	0.4	81	6	I40754	I40754 Sequence 85	C 447	20.6	0.4	51	6	AX165725	AX165725 Sequence
C 375	20.8	0.4	81	14	AF166789	AF166789 Hepatitis	C 448	20.6	0.4	51	6	E22365	E22365 Dna encodin
C 376	20.8	0.4	83	6	AX335957	AX335957 Sequence	C 449	20.6	0.4	51	6	AX162674	AX162674 Sequence
C 377	20.8	0.4	83	6	AX241021	AX241021 Sequence	C 450	20.6	0.4	51	6	AX162465	AX162465 Sequence
C 378	20.8	0.4	83	6	AX335957	AX335957 Sequence	C 451	20.6	0.4	51	6	AX165725	AX165725 Sequence
C 379	20.8	0.4	83	6	I36506	I36506 Sequence 5	C 452	20.6	0.4	51	6	E04184	E04184 Single stra
C 380	20.8	0.4	83	6	168832	168832 Sequence 93	C 453	20.6	0.4	51	6	ARI92735	ARI92735 Sequence
C 381	20.8	0.4	84	6	AR014622	AR014622 Sequence	C 454	20.6	0.4	51	6	E22365	E22365 Dna encodin
C 382	20.8	0.4	84	6	AR014623	AR014623 Sequence	C 455	20.6	0.4	51	6	AF357380	AF357380 Mus muscu
C 383	20.8	0.4	84	6	AX435976	AX435976 Sequence	C 456	20.6	0.4	51	6	AX485064	AX485064 Sequence
C 384	20.8	0.4	84	6	BD010414	BD010414 ChimERIC	C 457	20.6	0.4	51	6	AX485219	AX485219 Sequence
C 385	20.8	0.4	84	6	BD010415	BD010415 ChimERIC	C 458	20.6	0.4	51	6	AX485346	AX485346 Sequence
C 386	20.8	0.4	84	6	I26759	I26759 Sequence 88	C 459	20.6	0.4	51	6	AX485442	AX485442 Sequence
C 387	20.8	0.4	84	6	I26759	I26759 Sequence 89	C 460	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 388	20.8	0.4	84	14	ATH505735	ATH505735 Arabidops	C 461	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 389	20.8	0.4	84	14	HIV1P74V4R	HIV1P74V4R Sequence	C 462	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 390	20.8	0.4	85	6	AX099459	AX099459 Sequence	C 463	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 391	20.8	0.4	85	6	AX436009	AX436009 Sequence	C 464	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 392	20.8	0.4	86	6	AX203294	AX203294 Sequence	C 465	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 393	20.8	0.4	86	6	AX435997	AX435997 Sequence	C 466	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 394	20.8	0.4	86	6	AX436010	AX436010 Sequence	C 467	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 395	20.8	0.4	86	14	HIVPOLAG	HIVPOLAG Sequence	C 468	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 396	20.8	0.4	87	14	AX179367	AX179367 Sequence	C 469	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 397	20.8	0.4	87	14	A75439	A75439 Human Immun	C 470	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 398	20.8	0.4	89	6	A78418	A78418 Sequence 11	C 471	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 399	20.8	0.4	89	6	AX094087	AX094087 Sequence	C 472	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 400	20.8	0.4	90	1	STABLAZA	STABLAZA Sequence	C 473	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 401	20.8	0.4	90	6	AR077647	AR077647 Sequence	C 474	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 402	20.8	0.4	90	6	AX322428	AX322428 Sequence	C 475	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 403	20.8	0.4	90	9	HUMICMFA	HUMICMFA Sequence	C 476	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 404	20.8	0.4	90	14	E11248280	E11248280 Sequence	C 477	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 405	20.8	0.4	91	3	AF166145	AF166145 ChimERIC	C 478	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 406	20.8	0.4	91	4	BTU19470	BTU19470 Bos tauris	C 479	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 407	20.8	0.4	91	4	CHU19477	CHU19477 Capra hircu	C 480	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 408	20.8	0.4	92	14	HIVPOLAE	HIVPOLAE Sequence	C 481	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 409	20.8	0.4	93	6	BD003045	BD003045 Sequence	C 482	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 410	20.8	0.4	95	6	BD003045	BD003045 Sequence	C 483	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 411	20.8	0.4	95	6	BD003045	BD003045 Sequence	C 484	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 412	20.8	0.4	96	11	G12071	G12071 H. sapiens	C 485	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 413	20.8	0.4	96	11	HSC124EH4	HSC124EH4 Sequence	C 486	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 414	20.8	0.4	97	3	AY009547	AY009547 Boophilus	C 487	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 415	20.8	0.4	97	6	AR014605	AR014605 Sequence	C 488	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 416	20.8	0.4	97	6	AR014607	AR014607 Sequence	C 489	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 417	20.8	0.4	97	6	AR014617	AR014617 Sequence	C 490	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 418	20.8	0.4	97	6	AR014621	AR014621 Sequence	C 491	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 419	20.8	0.4	97	6	AR094798	AR094798 Sequence	C 492	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 420	20.8	0.4	97	6	BD010397	BD010397 ChimERIC	C 493	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 421	20.8	0.4	97	6	AR165457	AR165457 Sequence	C 494	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 422	20.8	0.4	97	6	BD010397	BD010397 ChimERIC	C 495	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 423	20.8	0.4	97	6	BD010409	BD010409 ChimERIC	C 496	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 424	20.8	0.4	97	6	I26746	I26746 Sequence 38	C 497	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 425	20.8	0.4	97	6	I26748	I26748 Sequence 42	C 498	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 426	20.8	0.4	98	6	AX039308	AX039308 Sequence	C 499	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 427	20.8	0.4	98	6	AX039517	AX039517 Sequence	C 500	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 428	20.8	0.4	98	6	E26102	E26102 Novel DNA f	C 501	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 429	20.8	0.4	98	10	MMV81N28	MMV81N28 Sequence	C 502	20.6	0.4	51	6	AX485489	AX485489 Sequence
C 430	20.8	0.4	98	10	MMV81N28	MMV81N28 Sequence	C 503	20.6	0.4	51	6	AX485489	AX485489 Sequence



C 504	20.6	0.4	89	8	AF001068	AF001068 GigaSpore
C 505	20.6	0.4	89	9	HS4230050	AJ230050 Homo sapi
C 506	20.6	0.4	90	6	AX451463	AX451463 Sequence
C 507	20.6	0.4	90	10	MUSIGRW2	M00548 mouse 19 ka
C 508	20.6	0.4	90	12	SYNDEL341	M10684 X.laeviis DN
C 509	20.6	0.4	90	17	HSDEC0317	X85354 H.sapiens t
C 510	20.6	0.4	91	6	AR072979	AR072979 Sequence
C 511	20.6	0.4	91	10	MUSATC2B11	M95510 Mus musculu
C 512	20.6	0.4	92	9	HUMMCA04	M95510 Human mediu
C 513	20.6	0.4	94	6	AX366494	AX366494 Sequence
C 514	20.6	0.4	96	6	A44582	A44582 Sequence 18
C 515	20.6	0.4	96	10	RATRADC10	L32996 Rat aromat
C 516	20.6	0.4	96	11	G16140	G16140 SMS2675 Br
C 517	20.6	0.4	97	11	AF247507	AF247507 Strongylo
C 518	20.6	0.4	97	11	AL773278	AL773278 Arabidops
C 519	20.6	0.4	97	11	AL773280	AL773280 Arabidops
C 520	20.6	0.4	97	11	AL773283	AL773283 Arabidops
C 521	20.6	0.4	97	11	AL773286	AL773286 Arabidops
C 522	20.6	0.4	98	6	AX192825	AX192825 Sequence
C 523	20.6	0.4	100	6	AX3830	AX3830 Sequence 4
C 524	20.6	0.4	100	6	A43845	A43845 Sequence 19
C 525	20.6	0.4	100	6	I17407	I17407 Sequence 4
C 526	20.6	0.4	100	6	I17422	I17422 Sequence 19
C 527	20.6	0.4	100	9	AF062779	AF062779 Glycine m
C 528	20.6	0.4	100	9	AJ08118	AJ08118 Homo sapi
C 529	20.6	0.4	100	14	POL3BRA	P00263 Human polio
C 530	20.6	0.4	100	6	A65366	A65366 Sequence 2
C 531	20.6	0.4	45	6	AX490814	AX490814 Sequence
C 532	20.6	0.4	51	6	AX158827	AX158827 Sequence
C 533	20.6	0.4	51	6	AX163076	AX163076 Sequence
C 534	20.6	0.4	57	6	AX37072	AX37072 Sequence 15
C 535	20.6	0.4	57	6	E15476	E15476 primer 7/1
C 536	20.6	0.4	57	6	E15476	E15476 primer 7/1
C 537	20.6	0.4	59	6	AX341922	AX341922 Sequence
C 538	20.6	0.4	60	6	AX139536	AX139536 Sequence
C 539	20.6	0.4	62	6	AX484256	AX484256 Sequence
C 540	20.6	0.4	65	6	AX485005	AX485005 Sequence
C 541	20.6	0.4	65	6	AX485830	AX485830 Sequence
C 542	20.6	0.4	65	6	AX485885	AX485885 Sequence
C 543	20.6	0.4	68	14	MH019937	U19937 Mouse hepat
C 544	20.6	0.4	69	6	I16689	I16689 Sequence 29
C 545	20.6	0.4	69	6	I16942	I16942 Sequence 29
C 546	20.6	0.4	69	11	G38355	G38355 st638 Misce
C 547	20.6	0.4	71	6	E34286	E34286 Environment
C 548	20.6	0.4	71	6	E34286	E34286 Environment
C 549	20.6	0.4	72	8	PBE230490	AJ240490 Physconia
C 550	20.6	0.4	73	6	A19088	A19088 Nucleotide
C 551	20.6	0.4	73	6	A19087	A19087 Nucleotide
C 552	20.6	0.4	74	6	A19089	A19089 Nucleotide
C 553	20.6	0.4	74	6	A19089	A19089 Nucleotide
C 554	20.6	0.4	75	1	SA073399	SA073399 Saccharom
C 555	20.6	0.4	75	3	AX014015	AX014015 Adineta v
C 556	20.6	0.4	75	6	AX107661	AX107661 Sequence
C 557	20.6	0.4	75	9	S70579	S70579 Homo sapien
C 558	20.6	0.4	76	6	AR042692	AR042692 Sequence
C 559	20.6	0.4	76	6	AR064825	AR064825 Sequence
C 560	20.6	0.4	76	6	AR125951	AR125951 Sequence
C 561	20.6	0.4	76	6	AX028738	AX028738 Sequence
C 562	20.6	0.4	76	6	AX028738	AX028738 Sequence
C 563	20.6	0.4	76	6	AX028738	AX028738 Sequence
C 564	20.6	0.4	77	8	MISC41	MISC41 Sequence 20
C 565	20.6	0.4	77	8	MISC41	MISC41 Sequence 20
C 566	20.6	0.4	77	8	MISC41	MISC41 Sequence 20
C 567	20.6	0.4	78	3	AY013952	AY013952 Eupripar
C 568	20.6	0.4	78	3	AY013958	AY013958 Habrotrac
C 569	20.6	0.4	78	3	AY014000	AY014000 Habrotrac
C 570	20.6	0.4	78	10	MUSCAXA	M37591 Mouse T cel
C 571	20.6	0.4	79	6	AX164120	AX164120 Sequence
C 572	20.6	0.4	80	5	AF117288	AF117288 Gallus ga
C 573	20.6	0.4	80	5	AF117288	AF117288 Gallus ga
C 574	20.6	0.4	81	14	AF155884	AF155884 HTV-1 iso
C 575	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 576	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 577	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 578	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 579	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 580	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 581	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 582	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 583	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 584	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 585	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 586	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 587	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 588	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 589	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 590	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 591	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 592	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
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C 650	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
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C 655	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
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C 674	20.6	0.4	81	14	AF221297	AF221297 Hepatitis
C 675	20.6	0.4	81			

C 650	20.2	0.4	51	6	AX116841	Sequence	723	20.2	0.4	96	10	RATPRO05	L00376 Rat skel
C 651	20.2	0.4	51	6	AX163176	Sequence	724	20.2	0.4	96	11	HS186X67	S25095 H. sapiens
C 652	20.2	0.4	51	6	AX165692	Sequence	725	20.2	0.4	97	8	S52653	S52653 pty2-pre-t
C 653	20.2	0.4	60	6	AR0179559	Sequence	726	20.2	0.4	98	6	AR087170	AR087170 Sequence
C 654	20.2	0.4	63	6	AR031249	Sequence	727	20.2	0.4	98	6	E36069	E36069 Higher-ord
C 655	20.2	0.4	63	6	AR075297	Sequence	728	20.2	0.4	98	6	I49625	I49625 Sequence
C 656	20.2	0.4	63	6	AR099956	Sequence	729	20.2	0.4	98	6	171467	171467 Sequence
C 657	20.2	0.4	63	6	AR169261	Sequence	730	20.2	0.4	99	3	AF343561	AF343561 Acantamo
C 658	20.2	0.4	63	6	AR183595	Sequence	731	20.2	0.4	99	3	HSPETS1	X7262 Haliclon
C 659	20.2	0.4	63	9	AF189477	Sequence	732	20.2	0.4	99	8	AF318055	AF318055 Sambucus
C 660	20.2	0.4	65	6	AX484349	Sequence	733	20.2	0.4	99	8	S52652	S52652 pty1-pre-t
C 661	20.2	0.4	65	6	AX485855	Sequence	734	20.2	0.4	99	9	AF005957	AF005957 Homo sapi
C 662	20.2	0.4	65	6	AX485925	Sequence	735	20.2	0.4	99	14	PCSVS15	K02085 Simian sarc
C 663	20.2	0.4	65	6	AX485926	Sequence	736	20.2	0.4	99	14	PCSVS15A	M12923 Simian sarc
C 664	20.2	0.4	65	6	AX486115	Sequence	737	20.2	0.4	100	1	ECOTNDCA	M31528 E. coli DNA
C 665	20.2	0.4	65	10	MUSPCKGPEC	Sequence	738	20.2	0.4	100	6	AX379183	AX379183 Sequence
C 666	20.2	0.4	66	9	HSU91195	Sequence	739	20.2	0.4	100	11	AR07535	AR07535 Arabidops
C 667	20.2	0.4	67	3	AF177249	Sequence	740	20.2	0.4	100	11	G32918	G32918 A009W25 Hum
C 668	20.2	0.4	69	6	AR007248	Sequence	741	20.2	0.4	100	11	AR07535	AR07535 Human chrom
C 669	20.2	0.4	69	6	AR012463	Sequence	742	20.2	0.4	100	11	HUMSXA149	L14972 Human chrom
C 670	20.2	0.4	69	6	AR020291	Sequence	743	20.2	0.4	38	6	AR194938	AR194938 Sequence
C 671	20.2	0.4	69	6	AR062452	Sequence	744	20.2	0.4	38	6	BD006438	BD006438 Compounds
C 672	20.2	0.4	69	6	AR109312	Sequence	745	20.2	0.4	38	6	BD006558	BD006558 Compounds
C 673	20.2	0.4	69	6	AR109312	Sequence	746	20.2	0.4	40	6	AR142030	AR142030 Sequence
C 674	20.2	0.4	69	6	AR170034	Sequence	747	20.2	0.4	40	6	159897	159897 Sequence
C 675	20.2	0.4	69	6	AX193362	Sequence	748	20.2	0.4	40	6	168066	168066 Sequence
C 676	20.2	0.4	69	6	I27738	Sequence	749	20.2	0.4	40	6	168066	168066 Sequence
C 677	20.2	0.4	69	6	I27738	Sequence	750	20.2	0.4	40	6	168066	168066 Sequence
C 678	20.2	0.4	69	6	AR007247	Sequence	751	20.2	0.4	41	6	AR009854	AR009854 Sequence
C 679	20.2	0.4	71	6	AR062451	Sequence	752	20.2	0.4	45	6	AR17057	AR17057 Sequence
C 680	20.2	0.4	71	6	AR170033	Sequence	753	20.2	0.4	45	6	AR014432	AR014432 Sequence
C 681	20.2	0.4	71	6	AR170460	Sequence	754	20.2	0.4	45	6	111875	111875 Sequence
C 682	20.2	0.4	71	6	I27737	Sequence	755	20.2	0.4	45	6	AX378294	AX378294 Sequence
C 683	20.2	0.4	72	8	NEUMTGA	Sequence	756	20.2	0.4	45	6	AR032581	AR032581 Sequence
C 684	20.2	0.4	73	6	AL9092	Sequence	757	20.2	0.4	48	6	AR0209245	AR0209245 Sequence
C 685	20.2	0.4	74	6	AL9091	Sequence	758	20.2	0.4	48	6	I29321	I29321 Sequence
C 686	20.2	0.4	75	8	NEUMTRA	Sequence	759	20.2	0.4	48	6	190995	190995 Sequence
C 687	20.2	0.4	75	8	NEUMTRA	Sequence	760	20.2	0.4	50	6	AX162086	AX162086 Sequence
C 688	20.2	0.4	75	9	AF043843	Sequence	761	20.2	0.4	51	6	AX156866	AX156866 Sequence
C 689	20.2	0.4	76	5	AF043844	Sequence	762	20.2	0.4	51	6	AX158150	AX158150 Sequence
C 690	20.2	0.4	76	5	S67412	Sequence	763	20.2	0.4	51	6	AX160456	AX160456 Sequence
C 691	20.2	0.4	78	8	AF374443	Sequence	764	20.2	0.4	51	6	AX160667	AX160667 Sequence
C 692	20.2	0.4	79	5	S67416	Sequence	765	20.2	0.4	51	6	AX160667	AX160667 Sequence
C 693	20.2	0.4	80	5	S67415	Sequence	766	20.2	0.4	51	6	AX160667	AX160667 Sequence
C 694	20.2	0.4	81	9	F327658S33	Sequence	767	20.2	0.4	51	6	AX160928	AX160928 Sequence
C 695	20.2	0.4	81	9	HUMTCRBD	Sequence	768	20.2	0.4	51	6	AX161269	AX161269 Sequence
C 696	20.2	0.4	82	9	HUMTCRBD	Sequence	769	20.2	0.4	51	6	AX199320	AX199320 Sequence
C 697	20.2	0.4	83	6	AX240981	Sequence	770	20.2	0.4	51	6	AX203978	AX203978 Sequence
C 698	20.2	0.4	83	10	AF357454	Sequence	771	20.2	0.4	54	6	AR081883	AR081883 Sequence
C 699	20.2	0.4	84	6	AR014637	Sequence	772	20.2	0.4	54	6	AR159917	AR159917 Sequence
C 700	20.2	0.4	84	6	BD010419	Sequence	773	20.2	0.4	55	14	HIV1045027	HIV1045027 Sequence
C 701	20.2	0.4	84	6	I26742	Sequence	774	20.2	0.4	55	14	HIV1045047	HIV1045047 Sequence
C 702	20.2	0.4	86	6	AX078800	Sequence	775	20.2	0.4	55	14	HIV1045049	HIV1045049 Sequence
C 703	20.2	0.4	87	4	AX112767	Sequence	776	20.2	0.4	55	14	HIV1045051	HIV1045051 Sequence
C 704	20.2	0.4	87	6	AR055088	Sequence	777	20.2	0.4	55	14	HIV1045055	HIV1045055 Sequence
C 705	20.2	0.4	87	6	AR156337	Sequence	778	20.2	0.4	55	14	HIV1045057	HIV1045057 Sequence
C 706	20.2	0.4	89	3	OFAB1WB3P	Sequence	779	20.2	0.4	55	14	HIV1045063	HIV1045063 Sequence
C 707	20.2	0.4	89	5	RCSCRNA	Sequence	780	20.2	0.4	55	14	HIV1045067	HIV1045067 Sequence
C 708	20.2	0.4	90	5	XX082796	Sequence	781	20.2	0.4	55	14	HIV1045071	HIV1045071 Sequence
C 709	20.2	0.4	90	6	AR072980	Sequence	782	20.2	0.4	55	14	HIV1045075	HIV1045075 Sequence
C 710	20.2	0.4	92	9	HSKRLX11A	Sequence	783	20.2	0.4	55	14	HIV1045079	HIV1045079 Sequence
C 711	20.2	0.4	95	6	AR140887	Sequence	784	20.2	0.4	55	14	HIV1045087	HIV1045087 Sequence
C 712	20.2	0.4	95	6	AR150837	Sequence	785	20.2	0.4	55	14	HIV1045091	HIV1045091 Sequence
C 713	20.2	0.4	95	6	155715	Sequence	786	20.2	0.4	55	14	HIV1045093	HIV1045093 Sequence
C 714	20.2	0.4	95	6	167947	Sequence	787	20.2	0.4	55	14	AX358702	AX358702 Sequence
C 715	20.2	0.4	95	6	190168	Sequence	788	20.2	0.4	56	6	AX358703	AX358703 Sequence
C 716	20.2	0.4	95	6	HSU29110	Sequence	789	20.2	0.4	56	6	AX358703	AX358703 Sequence
C 717	20.2	0.4	95	10	MMV51N27	Sequence	790	20.2	0.4	58	9	HUMCLSC	HUMCLSC Sequence
C 718	20.2	0.4	95	10	ECOC625	Sequence	791	20.2	0.4	58	9	HUMCLSC	HUMCLSC Sequence
C 719	20.2	0.4	96	1	AY006145	Sequence	792	20.2	0.4	58	9	HUMCLSC	HUMCLSC Sequence
C 720	20.2	0.4	96	9	AY006145	Sequence	793	20.2	0.4	58	9	HUMCLSC	HUMCLSC Sequence
C 721	20.2	0.4	96	9	AY006145	Sequence	794	20.2	0.4	58	9	HUMCLSC	HUMCLSC Sequence
C 722	20.2	0.4	96	9	AY006145	Sequence	795	20.2	0.4	58	9	HUMCLSC	HUMCLSC Sequence

C 796	20	0.4	59	6	AX358709	AX358709 Sequence	869	20	0.4	91	4	BTU19471	U19471 Bos taurus
C 797	20	0.4	59	6	AX358710	AX358710 Sequence	C 870	20	0.4	91	6	AX244617	AX244617 Sequence
C 798	20	0.4	59	6	AX358715	AX358715 Sequence	C 871	20	0.4	91	6	AX244617	AX244617 Sequence
C 799	20	0.4	59	6	AX358716	AX358716 Sequence	C 872	20	0.4	92	6	E05823	E05823 DNA encodin
C 800	20	0.4	60	6	AR068207	AR068207 Sequence	C 873	20	0.4	93	5	XMO82800	XMO82800 Xiphophorus
C 801	20	0.4	60	6	AR076959	AR076959 Sequence	C 874	20	0.4	93	6	ARI74921	ARI74921 Sequence
C 802	20	0.4	60	6	AR078792	AR078792 Sequence	C 875	20	0.4	93	6	AX084756	AX084756 Sequence
C 803	20	0.4	61	6	AR078792	AR078792 Sequence	C 876	20	0.4	93	6	AX282691	AX282691 Sequence
C 804	20	0.4	61	6	AR138413	AR138413 Sequence	C 877	20	0.4	93	6	HSRNP2509	HSRNP2509 Human renal
C 805	20	0.4	62	6	AR1371	AR1371 Repeat nucl	C 878	20	0.4	93	10	MMU26249	MMU26249 Mus musculus
C 806	20	0.4	63	6	AX037305	AX037305 Sequence	C 879	20	0.4	94	5	AF044762	AF044762 Phylosco
C 807	20	0.4	64	6	AX482832	AX482832 Sequence	C 880	20	0.4	94	6	AR205582	AR205582 Sequence
C 808	20	0.4	65	6	AX484244	AX484244 Sequence	C 881	20	0.4	94	6	AX076600	AX076600 Sequence
C 809	20	0.4	65	6	AX484729	AX484729 Sequence	C 882	20	0.4	95	3	LEIKPMFEA	LEIKPMFEA L. tarentola
C 810	20	0.4	65	6	AX485562	AX485562 Sequence	C 883	20	0.4	95	6	AR041085	AR041085 Sequence
C 811	20	0.4	65	6	AX486142	AX486142 Sequence	C 884	20	0.4	95	6	AR050589	AR050589 Sequence
C 812	20	0.4	65	6	AX486584	AX486584 Sequence	C 885	20	0.4	95	6	AR060693	AR060693 Sequence
C 813	20	0.4	67	6	AX486584	AX486584 Sequence	C 886	20	0.4	95	6	AR063126	AR063126 Sequence
C 814	20	0.4	67	6	AX486584	AX486584 Sequence	C 887	20	0.4	95	6	AR117015	AR117015 Sequence
C 815	20	0.4	68	6	AX486584	AX486584 Sequence	C 888	20	0.4	95	6	HSRNP1	HSRNP1 Human DNA f
C 816	20	0.4	68	6	AX486584	AX486584 Sequence	C 889	20	0.4	95	6	AF411999	AF411999 Formica e
C 817	20	0.4	70	6	AR207788	AR207788 Sequence	C 890	20	0.4	96	3	AX039237	AX039237 Sequence
C 818	20	0.4	70	6	AR207788	AR207788 Sequence	C 891	20	0.4	96	6	AX039237	AX039237 Sequence
C 819	20	0.4	72	8	CRMETTRNA	CRMETTRNA	C 892	20	0.4	96	6	AX039477	AX039477 Sequence
C 820	20	0.4	73	5	AF301558	AF301558 Bucephala	C 893	20	0.4	96	6	AX039478	AX039478 Sequence
C 821	20	0.4	73	5	AR091365	AR091365 Sequence	C 894	20	0.4	96	6	AX134835	AX134835 Sequence
C 822	20	0.4	74	6	AR93124	AR93124 Sequence	C 895	20	0.4	96	6	AX134835	AX134835 Sequence
C 823	20	0.4	74	6	AR134559	AR134559 Sequence	C 896	20	0.4	96	6	AX134835	AX134835 Sequence
C 824	20	0.4	74	6	AR134559	AR134559 Sequence	C 897	20	0.4	96	6	AX134835	AX134835 Sequence
C 825	20	0.4	75	6	AR043921	AR043921 Sequence	C 898	20	0.4	96	6	AX134835	AX134835 Sequence
C 826	20	0.4	75	6	HSLS90	HSLS90	C 899	20	0.4	96	6	AX135043	AX135043 Sequence
C 827	20	0.4	76	9	HSLS90	HSLS90	C 900	20	0.4	96	6	AX135043	AX135043 Sequence
C 828	20	0.4	76	9	HSLS90	HSLS90	C 901	20	0.4	96	6	AX135043	AX135043 Sequence
C 829	20	0.4	76	9	HSLS90	HSLS90	C 902	20	0.4	96	6	AX135043	AX135043 Sequence
C 830	20	0.4	79	6	AX233554	AX233554 Sequence	C 903	20	0.4	96	6	AX135043	AX135043 Sequence
C 831	20	0.4	80	6	E02438	E02438 DNA encodin	C 904	20	0.4	98	6	AF263206	AF263206 Sequence
C 832	20	0.4	80	6	E02442	E02442 DNA encodin	C 905	20	0.4	98	6	AX210035	AX210035 Sequence
C 833	20	0.4	80	6	E02446	E02446 DNA encodin	C 906	20	0.4	99	6	AS0274	AS0274 HSMC27G04
C 834	20	0.4	81	6	AR062736	AR062736 Sequence	C 907	20	0.4	100	6	AR142897	AR142897 Sequence
C 835	20	0.4	81	6	AR051511	AR051511 Sequence	C 908	20	0.4	100	6	AX260734	AX260734 Sequence
C 836	20	0.4	82	6	AR072651	AR072651 Sequence	C 909	20	0.4	100	6	HUMIGJHC	HUMIGJHC Human Ig ge
C 837	20	0.4	82	6	AR073196	AR073196 Sequence	C 910	20	0.4	100	6	AX158178	AX158178 Sequence
C 838	20	0.4	82	6	AR051521	AR051521 Sequence	C 911	20	0.4	100	6	AX158178	AX158178 Sequence
C 839	20	0.4	82	6	AR051521	AR051521 Sequence	C 912	20	0.4	100	6	AX158178	AX158178 Sequence
C 840	20	0.4	84	6	AR072661	AR072661 Sequence	C 913	20	0.4	100	6	AX158178	AX158178 Sequence
C 841	20	0.4	84	6	AR072661	AR072661 Sequence	C 914	20	0.4	100	6	AX158178	AX158178 Sequence
C 842	20	0.4	84	6	AR072661	AR072661 Sequence	C 915	20	0.4	100	6	AX158178	AX158178 Sequence
C 843	20	0.4	84	6	AR072661	AR072661 Sequence	C 916	20	0.4	100	6	AX158178	AX158178 Sequence
C 844	20	0.4	84	6	AR072661	AR072661 Sequence	C 917	20	0.4	100	6	AX158178	AX158178 Sequence
C 845	20	0.4	84	6	AR072661	AR072661 Sequence	C 918	20	0.4	100	6	AX158178	AX158178 Sequence
C 846	20	0.4	84	6	AR072661	AR072661 Sequence	C 919	20	0.4	100	6	AX158178	AX158178 Sequence
C 847	20	0.4	85	3	AX241048	AX241048 Sequence	C 920	20	0.4	100	6	AX158178	AX158178 Sequence
C 848	20	0.4	87	9	HSXARESO1	HSXARESO1	C 921	20	0.4	100	6	AX158178	AX158178 Sequence
C 849	20	0.4	87	9	HSXARESO1	HSXARESO1	C 922	20	0.4	100	6	AX158178	AX158178 Sequence
C 850	20	0.4	87	9	HSXARESO1	HSXARESO1	C 923	20	0.4	100	6	AX158178	AX158178 Sequence
C 851	20	0.4	87	9	HSXARESO1	HSXARESO1	C 924	20	0.4	100	6	AX158178	AX158178 Sequence
C 852	20	0.4	88	1	HEA62U	HEA62U	C 925	20	0.4	100	6	AX158178	AX158178 Sequence
C 853	20	0.4	88	6	AX465615	AX465615 Sequence	C 926	20	0.4	100	6	AX158178	AX158178 Sequence
C 854	20	0.4	88	6	HSILGFR26	HSILGFR26	C 927	20	0.4	100	6	AX158178	AX158178 Sequence
C 855	20	0.4	88	6	AR045023	AR045023 Sequence	C 928	20	0.4	100	6	AX158178	AX158178 Sequence
C 856	20	0.4	89	6	IL18555	IL18555 Sequence	C 929	20	0.4	100	6	AX158178	AX158178 Sequence
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C 858	20	0.4	89	6	IL18555	IL18555 Sequence	C 931	20	0.4	100	6	AX158178	AX158178 Sequence
C 859	20	0.4	89	6	IL18555	IL18555 Sequence	C 932	20	0.4	100	6	AX158178	AX158178 Sequence
C 860	20	0.4	89	6	IL18555	IL18555 Sequence	C 933	20	0.4	100	6	AX158178	AX158178 Sequence
C 861	20	0.4	89	6	IL18555	IL18555 Sequence	C 934	20	0.4	100	6	AX158178	AX158178 Sequence
C 862	20	0.4	89	6	IL18555	IL18555 Sequence	C 935	20	0.4	100	6	AX158178	AX158178 Sequence
C 863	20	0.4	89	6	IL18555	IL18555 Sequence	C 936	20	0.4	100	6	AX158178	AX158178 Sequence
C 864	20	0.4	89	6	IL18555	IL18555 Sequence	C 937	20	0.4	100	6	AX158178	AX158178 Sequence
C 865	20	0.4	89	6	IL18555	IL18555 Sequence	C 938	20	0.4	100	6	AX158178	AX158178 Sequence
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C 867	20	0.4	89	6	IL18555	IL18555 Sequence	C 940	20	0.4	100	6	AX158178	AX158178 Sequence
C 868	20	0.4	89	6	IL18555	IL18555 Sequence	C 941	20	0.4	100	6	AX158178	AX158178 Sequence

942	19.8	0.4	70	6	AX347691	AX347691 Sequence
C 943	19.8	0.4	71	6	ARI40783	ARI40783 Sequence
C 944	19.8	0.4	71	6	193462	193462 Sequence 60
C 945	19.8	0.4	71	6	195089	195089 Sequence 60
946	19.8	0.4	72	6	AX363480	AX363480 Sequence
947	19.8	0.4	72	10	RATCKRP2	D1319 Rattus norv
948	19.8	0.4	72	12	SYN1718PS	M35460 Plasmid PRW
949	19.8	0.4	73	10	MYO403188	AI033188 M.musculi
C 950	19.8	0.4	74	6	A86634	A86634 Sequence 43
C 951	19.8	0.4	74	6	A86635	A86635 Sequence 44
C 952	19.8	0.4	74	6	ARI18843	ARI18843 Sequence 35
C 953	19.8	0.4	74	6	I06415	I06415 Sequence 4
954	19.8	0.4	75	6	A83284	A83284 Sequence 35
955	19.8	0.4	75	6	AR011553	AR011553 Sequence 4
C 956	19.8	0.4	75	6	AR051453	AR051453 Sequence 4
C 957	19.8	0.4	75	6	AR072593	AR072593 Sequence 4
C 958	19.8	0.4	75	6	AR073138	AR073138 Sequence 4
959	19.8	0.4	75	6	AX195253	AX195253 Sequence 4
960	19.8	0.4	75	6	AX241126	AX241126 Sequence 4
961	19.8	0.4	75	6	I18191	I18191 Sequence 42
962	19.8	0.4	75	14	MH019934	U19934 Mouse hepat
C 963	19.8	0.4	76	3	AF017049	AF017049 Plasmid
C 964	19.8	0.4	76	3	AY013972	AY013972 Drosophila
C 965	19.8	0.4	76	11	HUMUT628A	I30054 Human STS U
C 966	19.8	0.4	78	9	HS241956	AJ241956 Homo sapi
C 967	19.8	0.4	78	9	HUMTCATE	W23343 Homo sapien
C 968	19.8	0.4	79	6	AX381561	AX381561 Sequence
C 969	19.8	0.4	79	11	AL823769	AL823769 Arabidops
C 970	19.8	0.4	80	3	DROR51584	M0167 D.melanogas
C 971	19.8	0.4	80	3	DROR51586	M1539 D.melanogas
972	19.8	0.4	80	6	AX241111	AX241111 Sequence
973	19.8	0.4	80	6	AX287564	AX287564 Sequence
C 974	19.8	0.4	80	6	AX287565	AX287565 Sequence
C 975	19.8	0.4	80	6	I73619	I73619 Sequence 73
C 976	19.8	0.4	80	9	S64866S1	S64866 Hylobates s
977	19.8	0.4	81	1	BACRMAE	M15407 B.subtilis
C 978	19.8	0.4	81	6	AF043839	AF043839 Homo sapi
C 979	19.8	0.4	81	6	AF043839	M81941 Human CD34
C 980	19.8	0.4	81	9	HUMCD3454	AB089884 Notwalk v
C 981	19.8	0.4	81	14	AB089884	AF274846 Homo sapi
C 982	19.8	0.4	82	9	AF274846	AJ230619 Rattus no
C 983	19.8	0.4	82	10	RNO230619	AR042802 Sequence
C 984	19.8	0.4	83	6	AR042802	L47708 Homo sapien
C 985	19.8	0.4	83	9	HUMFON1112	I11718 Sequence 4
986	19.8	0.4	84	6	I11718	I11718 Sequence 4
987	19.8	0.4	84	6	I17334	I17334 Sequence 4
988	19.8	0.4	84	6	I43850	I43850 Sequence 4
C 989	19.8	0.4	84	10	MUSIGRCOV	M30432 Mouse 19 un
C 990	19.8	0.4	85	6	AX025268	AX025268 Sequence
C 991	19.8	0.4	85	9	S7542506	S75436 collagen ty
C 992	19.8	0.4	86	6	AX039312	AX039312 Sequence
C 993	19.8	0.4	86	6	AX039321	AX039321 Sequence
C 994	19.8	0.4	86	6	AX240975	AX240975 Sequence
995	19.8	0.4	86	11	G68158	G68158 D7S3169 (34
996	19.8	0.4	88	6	AR043969	AR043969 Sequence
997	19.8	0.4	88	6	AR073502	AR073502 Sequence
998	19.8	0.4	88	6	ARI46938	ARI46938 Sequence
999	19.8	0.4	88	6	AX022112	AX022112 Sequence
1000	19.8	0.4	88	6	AX039313	AX039313 Sequence

## ALIGNMENTS

RESULT 1  
LOCUS DDIDDKD  
DEFINITION D discoidium protein kinase 4 gene, partial cds.  
ACCESSION M59747.1 GI:167723  
VERSION M59747.1  
KEYWORDS protein kinase 4.  
SOURCE Dictyostelium discoidium (strain AX-3) DNA.  
ORGANISM Dictyostelium discoidium

REFERENCE  
AUTHORS Haribabu, B. and Doltin, R. P.  
TITLE Identification of a protein kinase multigene family of Dictyostelium discoidium: molecular cloning and expression of a cDNA encoding a developmentally regulated protein kinase  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1115-1119 (1991)  
MEDLINE 91142122  
PUBMED 1996312  
FEATURES  
source location/Qualifiers  
1..87  
/organism="Dictyostelium discoidium"  
/strain="AX-3"  
/db\_xref="taxon:44689"  
CDS  
1..>87  
/codon\_start=1  
/product="protein kinase 4"  
/protein\_id="AAA3189.1"  
/db\_xref="GI:167724"  
/translation="NLIIDYGHKIDFGFAKRTTNTSMC"

BASE COUNT  
ORIGIN  
36 a 12 c 14 g 25 t

Query Match  
Best Local Similarity 59.5%; Pred. No. 2.5e+04;  
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 4051 AATATCTTCCTTACCTGATTCGATTATCAACGAGGAGTTTGGATGTCAGTAAAG 4110  
Db 1 AATCTATTATGATGATCATATGATGATTTAAGCTACAGATTTTGGATTTGAAAAAGA 60  
QY 4111 CTCAAAACATGATCCACATG 4134  
Db 61 ATCACAGAGATACCAAAAGTATG 84

RESULT 2  
LOCUS AR007403/c 100 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 4 from patent US 5750497.  
ACCESSION AR007403  
VERSION AR007403.1 GI:3966887  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 100)  
AUTHORS Havelund, S., Halstr. o slashed. m, J., Jonassen, I., Andersen, A. Sloth.  
TITLE Acylated Insulin  
JOURNAL Patent: US 5750497-A 4 12-MAY-1998;  
FEATURES  
source location/Qualifiers  
1..100  
/organism="unknown"  
BASE COUNT  
ORIGIN  
29 a 22 c 23 g 26 t

Query Match  
Best Local Similarity 55.6%; Pred. No. 2.3e+05;  
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 4469 AAGATGAGGAGCTTACATATGACTTGAATAATCTCTTAATCACTACTGATGTA 4528  
Db 97 AAGTCTGACGAGGCTAAGGATGATGTTGACACATCTGTACTTCTATCTCTTGTAC 38  
QY 4529 TATTACATTAAGACTGCTGAGAGCAG 4558  
Db 37 CAATTGAAACTACTGTCTTACACGAG 8

RESULT 3  
LOCUS AX381834/c 81 bp DNA linear PAT 18-MAR-2002  
AX381834

DEFINITION Sequence 772 from Patent WO0212280.  
 AX381834  
 VERSION AX381834.1 GI:19576656  
 KEYWORDS  
 SOURCE Homo sapiens  
 ORGANISM human.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 Pyle, R.A., Xu, J. and Secrist, H.  
 AUTHORS Compositions and methods for the therapy and diagnosis of colon  
 TITLE Cancer  
 JOURNAL Patent: WO 0212280-A 772 14-FEB-2002;  
 CORIXA CORPORATION (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 81  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 9 a 22 c 15 g 33 t 2 others  
 ORIGIN  
 Query Match 0.5%; Score 25.8; DB 6; Length 81;  
 Best local Similarity 57.0%; Pred. No. 2.6e+05;  
 Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  
 Oy 3723 CACCTGCATCAGCGTCGACCGGACCTGATGCGCATGAAGAGATTGCAATTCACACC 3782  
 Db 79 CACGACAGACGAGGTACCTTTGGGAGCAGAGAGCCATMAAAGTTCAAGTCAAAA 20  
 Oy 3783 TAATGACCATTAAGACTATC 3801  
 Db 19 AAAAAAAAAAGGCGCNC 1  
 RESULT 4  
 AF025984 96 bp DNA linear VRT 30-OCT-1997  
 AF025984  
 LOCUS Parilichthys dentatus lactate dehydrogenase (LDHA) gene, allele  
 DEFINITION POLDHA2, Intron 6.  
 ACCESSION AF025984  
 VERSION AF025984.1 GI:2570847  
 KEYWORDS  
 SOURCE Parilichthys dentatus.  
 ORGANISM Parilichthys dentatus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 Pleuronectoidae; Parilichthyidae; Parilichthys.  
 REFERENCE 1 (bases 1 to 96)  
 AUTHORS Quattro, J.M. and Jones, W.J.  
 TITLE Amplification Primers That Target Locus-Specific Introns in  
 TITLE Actinopterygian Fishes  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 96)  
 AUTHORS Quattro, J.M. and Jones, W.J.  
 TITLE Direct Submission  
 JOURNAL Submitted (32-SEP-1997) Biological Sciences, University of South  
 Carolina, Coker Life Sciences Building, Columbia, SC 29208, USA  
 FEATURES  
 source Location/Qualifiers  
 1. 96  
 /organism="Parilichthys dentatus"  
 /db\_xref="taxon:66718"  
 gene 1. 96 "LDHA"  
 /gene="LDHA"  
 /note="Lactate dehydrogenase gene"  
 /allele="POLDHA2"  
 1. 96  
 /gene="LDHA"  
 /number=6  
 BASE COUNT 24 a 22 c 20 g 30 t  
 ORIGIN  
 Query Match 0.5%; Score 25.4; DB 5; Length 96;

Best Local Similarity 64.4%; Pred. No. 3.4e+05;  
 Matches 38; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
 Oy 4423 GCCAGCGAGCTCTCCGACCATTCGTTGTGTCACAGATGAAGAGACCT 4481  
 Db 14 GTGCGACAATCTAGACGATTCATTACAAACAGTGTGAGTGAATGAGTCT 72  
 RESULT 5  
 AX486379 65 bp DNA linear PAT 16-AUG-2002  
 AX486379  
 LOCUS Sequence 3679 from Patent WO02053728.  
 DEFINITION  
 ACCESSION AX486379  
 VERSION AX486379.1 GI:22320595  
 KEYWORDS  
 SOURCE Candida albicans.  
 ORGANISM Candida albicans.  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 REFERENCE 1 Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.  
 AUTHORS Gene disruption methodologies for drug target discovery  
 TITLE Patent: WO 02053728-A 3679 11-JUL-2002;  
 JOURNAL Eli Lilly Pharmaceuticals, Inc. (US)  
 FEATURES  
 source Location/Qualifiers  
 1. 65  
 /organism="Candida albicans"  
 /db\_xref="taxon:5476"  
 BASE COUNT 14 a 5 c 22 g 24 t  
 ORIGIN  
 Query Match 0.5%; Score 25.2; DB 6; Length 65;  
 Best local Similarity 62.9%; Pred. No. 3.8e+05;  
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
 Oy 712 TATGGAGCTTCGCTGTTAGATAGAGATGTTTATGATGATCTAGTACAGAGG 771  
 Db 1 TTGGGACTTCAACTTTTAAGTGTGAGAGTGGCAGATGATGATAGAGTGG 60  
 Oy 772 CA 773  
 Db 61 GA 62  
 RESULT 6  
 AX033167 70 bp DNA linear BCT 21-SEP-2000  
 AX033167  
 LOCUS Sequence 3 from Patent WO0045176.  
 DEFINITION  
 ACCESSION AX033167  
 VERSION AX033167.1 GI:10280029  
 KEYWORDS  
 SOURCE Escherichia coli.  
 ORGANISM Escherichia coli.  
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 Escherichia.  
 REFERENCE 1 (bases 1 to 70)  
 AUTHORS Gallusser, A., Karl, J., Lill, H., Stahl, P., Krueger, K. and Borgya, A.  
 TITLE Method of identifying n-terminal propep  
 JOURNAL Patent: WO 0045176-A 03-AUG-2000;  
 GALUSSER, ANDREAS (DE); KARL, JOHANN (DE); LILL, HELMUT (DE);  
 STAHL, PETER (DE); KRUEGER, KERSTIN (DE); BORGYA, ANNETLESE (DE);  
 ROCHER, DIAGNOSTICS GmbH (DE)  
 FEATURES  
 source Location/Qualifiers  
 1. 70  
 /organism="Escherichia coli"  
 /db\_xref="taxon:562"  
 BASE COUNT 10 a 19 c 21 g 20 t  
 ORIGIN  
 Query Match 0.5%; Score 25.2; DB 1; Length 70;  
 Best local Similarity 62.9%; Pred. No. 3.8e+05;  
 Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY	1778	AGGCGGGCTGCTGATCGACGCACTACTTACCACTTATCTCGAGGAGTTCGAGGACT	1837
Db	8	AGGAGAGTCTGTTCAACCTGCACTGCACTTTCGACACTTTTACCTCGAGGTGTTACGCTGTTCC	67
QY	1838	TG 1839	
		68 TG 69	

RESULT 7			
AX033159	AX033159	70 bp	linear
LOCUS	Sequence 3 from Patent WO0045176.		
DEFINITION			
ACCESSION	AX033159		
VERSION	AX033159.1		
KEYWORDS	GI:10280023		
SOURCE			
ORGANISM	Escherichia coli.		
	Escherichia coli.		

REFERENCE	1 (bases 1 to 70)
AUTHORS	Gallusser,A., Karl,J., Lill,H., Stahl,P., Krueger,K. and Borgia,A
TITLE	Method of identifying n-terminal protpnp
JOURNAL	Patent: WO 0045176-A 3 03-AUG-2000;
FEATURES	GALLUSSER ANDREAS (DE) ; KARL JOHANN (DE) ; STAHL PETER (DE) ; KRUEGER KERSTIN (DE) ; ROCHE DIAGNOSTICS GMBH (DE) ; Location/Qualifiers 1..70 /organism="Escherichia coli" /db_xref="taxon:562"
BASE COUNT	10 a 19 c 21 g 20 t
ORIGIN	

Query Match	0.5%	Score 25.2	DB 6	Length 70
Best Local Similarity	62.9%	Pred. No. 3.8e+05		
Matches 39	Conservative 0	Mismatches 23	Indels 0	Gaps 0
1778	AGGCGCGCCTCTCATGACGACGACTACTACCAAGTTCATGCGAGAGGTTCTGTGAGGACT			1837
8	AGGAGGGCTGTTCACCTCGACGTTCCGAGACAGTTTACCTCGACGGTGTTCACCTGTTC			67
1838	TG 1839			
68	TG 69			

RESULT 8					
LOCUS	165769				
DEFINITION	165769	99 bp	DNA	linear	PAT 07-OCT-1997
ACCESSION	Sequence 5 from patent US 5668294.				
VERSION	165769				
KEYWORDS	165769.1	GI:2482339			
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 99)				
TITLE	Meagher,R.B. and Summers,A.O.				
JOURNAL	Metal resistance sequences and transgenic plants				
FEATURES	Patent: US 5668294-A 5 16-SEP-1997;				
source	location/Qualifiers				
	1..99				
	/organism="unknown"				
BASE COUNT	29 a	21 c	25 g	24 t	
ORIGIN					

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Query Match      0.58;   Score 25.2; DB 6; Length 99;
Best Local Similarity 54.3%; Pred. No. 3.9e+05;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3026 ATGTCTGACTAAATGTAGAGTGTACAGCACCAGTAGTGCGCATCAAGAT 3085
    | ||| |||| || ||| || ||||
```

Db 2 AAGACCCAGCTAAVAGGTGAAGCTGTACTGTCGATTTCCGATGGAAGCATTCGAAGTGC 6  
OY 3086 TTGATTTTTCACAGCAATGGAACCTGCCTTAT 3119  
||| | ||||| | ||||| ||  
Db 62 GTGAGCATTACTCAAGCAAGCCAAAGTTGGCTATAT 95

RESULT	9
RABPFKM18	
LOCUS	
DEFINITION	83 bp DNA linear
ACCESSION	M14473 J02702
VERSION	M14473.1 GI:165622
KEYWORDS	phosphofructokinase.
SEGMENT	18 of 22
SOURCE	Rabbit (New Zealand)
ORGANISM	Oryctolagus cuniculus
	DNA, clone lambda-Charon 4APK.
	MM 27-APR-1999

FEATURES	REFERENCE
AUTHORS	Seemungal, B. and Putney, S.D.
TITLE	1 (Phases 1 to 83)
JOURNAL	Lee, C.P., Kao, M.C., French, B.A., Putney, S.D. and Chang, S.H.
MEDLINE	The rabbit muscle phosphofructokinase gene. Implications for
PUBMED	protein structure, function, and tissue specificity
COMMENT	J. Biol. Chem. 262 (9), 4195-4199 (1987)
	87166033
	2951385
	Draft entry and computer-readable sequence for [1] kindly provided
	by S.H. Chang, 02-FEB-1987.

FEATURES	
source	Location/Qualifiers
intron	1..83 /organism="Oryctolagus cuniculus" /db_xref="taxon:9986" <1..15 /note="PFK intron Q" 16..77 /number=18 78..>83 /note="PFK intron R"
exon	23 a 27 g 20 t 13 c
intron	About 719 bp after segment 17.
BASE COUNT	
ORIGIN	

[illegible]

RESULT 10				
AX173377/c				
LOCUS	AX173377	92 bp	DNA	linear
DEFINITION	Sequence			PAT 03-JUL-2001
ACCESSION	AX173377			
VERSION	AX173377.1			
KEYWORDS	GI:14598152			
SOURCE				
ORGANISM	synthetic construct.			
	synthetic construct.			
	artificial sequences.			
REFERENCE	1 (bases 1 to 92)			
AUTHORS	Murphy, B.R., Collins, P.L., Schmidt, A.C., Durbin, A.P.,			
	Skidopoulos, M.H. and Tao, T.			
	Use of recombinant parainfluenza viruses (pIvs) as vectors to			
	protect against infection and disease caused by pIv and other human			
	pathogens			
	Patent: WO 01/24445-A 31 14-JUN-2001;			
JOURNAL	The Secretary of the Department of Health and Human Services (US)			
FEATURES	Location/Qualifiers			



ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 73)  
 AUTHORS Monckton,D.G. and Jeffreys,A.J.  
 TITLE Minisatellite 'isoallele' discrimination in pseudohomozygotes by single molecule PCR and variant repeat mapping  
 JOURNAL Genomics 11 (2), 465-467 (1991)  
 MEDLINE 92120671  
 PUBMED 1769661  
 REMARK GenBank staff at the National Library of Medicine created this entry [NCBI glibseq 76509] from the original journal article.  
 This sequence comes from Figure 2.  
 FEATURES  
 source location/Qualifiers  
 1..73  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /gene="D1S8"  
 /allele="A"  
 BASE COUNT 41 a 0 c 0 g 32 t  
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 Best Local Similarity 0.5%; Score 24.4; DB 9; Length 73;  
 Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
 Oy 4914 TGTATGCAAAAGGCTGATTCGAAATTTAGAAAAGGCTCTTTTTCATTAATGCT 4973  
 Db 72 TATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4973  
 Oy 4974 TTTATTT 4979  
 Db 12 TTTATTT 7  
 RESULT 16  
 DROTRANSIN/C  
 LOCUS DROTRANSIN 98 bp DNA linear INV 05-JAN-1994  
 DEFINITION Drosophila melanogaster DNA sequence, complete insertion sequence.  
 ACCESSION L20950.1 GI:304832  
 VERSION L20950.1 GI:304832  
 KEYWORDS insertion sequence.  
 SOURCE Drosophila melanogaster (individual isolate B20.3) DNA.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 REFERENCE 1 (bases 1 to 98)  
 AUTHORS Engels,W.R. and Johnson-Schlitz,D.M.  
 TITLE Deletion white allele. Transposase-induced derivative of white-hd80k17  
 JOURNAL Unpublished (1993)  
 REFERENCE 2 (bases 1 to 98)  
 AUTHORS Johnson-Schlitz,D.M. and Engels,W.R.  
 TITLE P-element-induced interallelic gene conversion of insertions and deletions in Drosophila melanogaster  
 JOURNAL Mol. Cell. Biol. 13 (11), 7006-7018 (1993)  
 MEDLINE 94019372  
 PUBMED 8413290  
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 source location/Qualifiers  
 1..98  
 /organism="Drosophila melanogaster"  
 /isolate="B20.3"  
 /db\_xref="taxon:7227"  
 BASE COUNT 37 a 2 c 1 g 58 t  
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 Query Match  
 Best Local Similarity 0.5%; Score 24.4; DB 3; Length 98;  
 Matches 46; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
 Oy 1362 TGTGACTCTTATTTATAGACCAATTTGTAGACAACAGCAGGAGGAGTTAAGAAA 1421

Db 85 TTTAAATTTTATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1443  
 Oy 1422 GTTAATTTTAAAGACTTCACAG 1443  
 Db 25 TTTAATTTAATAATAATCATG 4  
 RESULT 17  
 AR007408/C  
 LOCUS AR007408 100 bp DNA linear PAT 04-DEC-1998  
 DEFINITION Sequence 9 from patent US 5750497.  
 ACCESSION AR007408  
 VERSION AR007408.1 GI:3966892  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 100)  
 AUTHORS Havelund,S., Halstr.o slashed,m.J., Jonassen,I., Andersen,A.Sloch. and Markusen,J.  
 TITLE Acylated insulin  
 JOURNAL Patent: US 5750497-A 9 12-MAY-1998;  
 FEATURES  
 source location/Qualifiers  
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 /organism="unknown"  
 BASE COUNT 29 a 23 c 22 g 26 t  
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 Best Local Similarity 0.5%; Score 24.4; DB 6; Length 100;  
 Matches 49; Conservative 0; Mismatches 41; Indels 0; Gaps 0;  
 Oy 4469 AAGATGAAGCCTAGTAGAATATGACCTTGGAATTTCTTAATCACTACTGATGTA 4528  
 Db 97 AAGTCTGACGACGCTAAGGCTATCGTTGACACATGCTTACTTATCTGTTTGTAC 4528  
 Oy 4529 TATTTACATTAAGACTGCTGAGAACGAG 4558  
 Db 37 CATTGGAAACTACTGCTGTAGACGACAG 8  
 RESULT 18  
 AX486337  
 LOCUS AX486337 65 bp DNA linear PAT 16-AUG-2002  
 DEFINITION Sequence 3637 from Patent WO02053728.  
 ACCESSION AX486337  
 VERSION AX486337.1 GI:22320553  
 KEYWORDS  
 SOURCE Candida albicans.  
 ORGANISM Candida albicans  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 REFERENCE 1  
 AUTHORS Roemer,T., Jlang,B., Boone,C., Bussey,H. and Ohlsen,K.L.  
 TITLE Gene disruption methodologies for drug target discovery  
 JOURNAL Patent: WO 02053728-A 3637 11-JUL-2002;  
 MEDLINE  
 PUBMED  
 FEATURES  
 source location/Qualifiers  
 1..65  
 /organism="Candida albicans"  
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 BASE COUNT 8 a 12 c 13 g 32 t  
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 Query Match  
 Best Local Similarity 0.5%; Score 24.2; DB 6; Length 65;  
 Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
 Oy 4838 TTTTAATTCCTCTTTGTTGAGAGCAGCTGTAACCTTTTACCTTTTGTGTTGT 4897  
 Db 1 TTTTATGCTCTGCTTTCTTAACTGACCTCTATGCGCTTATTAAGATGTGTTGTGT 60



OY 4898 T 4898  
 DB 61 T 61

RESULT 19  
 LOCUS U92173 51 bp mRNA linear ROD 19-FEB-1998  
 DEFINITION Mus musculus clone 1c3 T cell receptor beta chain mRNA, partial cds.  
 ACCESSION U92173  
 VERSION U92173.1 GI:2894946  
 KEYWORDS  
 SOURCE Mus musculus.  
 ORGANISM Mus musculus; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS Johnston, S.L. and Wettstein, P.J.  
 TITLE T cell receptor diversity in CTLs specific for the CTT-1 and CTT-2 minor histocompatibility antigens  
 JOURNAL J. Immunol. 159 (6), 2606-2615 (1997)  
 MEDLINE 97444147  
 PUBMED 9300679  
 REFERENCES Johnston, S.L. and Wettstein, P.J.  
 DIRECT SUBMISSION  
 TITLE Submitted (06-MAR-1997) Immunology, Mayo Clinic, 200 1st St S.W., Rochester, MN 55905, USA  
 JOURNAL Location/Qualifiers

FEATURES  
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 /strain="C57BL/6"  
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 /db\_xref="GI:2894947"  
 /translation="YCTCSDPDYSGNTLYF"  
 BASE COUNT 12 a 13 c 11 g 15 t  
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Query Match 0.5%; Score 24; DB 10; Length 51;  
 Best Local Similarity 75.0%; Pred. No. 7.9e+05;  
 Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1513 GAATTCGATCCGATGGGCTTCAGATTATGTCAGT 1552  
 DB 41 GTATTTCGATACCTCTCGGATGACATGACGTCAGT 2

RESULT 20  
 LOCUS AX483371 65 bp DNA linear PAT 16-AUG-2002  
 DEFINITION Sequence 671 from Patent WO0205372.  
 ACCESSION AX483371  
 VERSION AX483371.1 GI:22317791  
 KEYWORDS  
 SOURCE Candida albicans.  
 ORGANISM Candida albicans; Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.

REFERENCE  
 AUTHORS Roemer, T., Jiang, B., Boone, C., Bussey, H. and Ohlsen, K.L.  
 TITLE Gene disruption methodologies for drug target discovery  
 JOURNAL Patent: WO 0205372-A 671 11-JUL-2002;  
 Biotra Pharmaceuticals, Inc. (US)  
 FEATURES  
 source 1..65  
 Location/Qualifiers

BASE COUNT 23 a 2 c 20 g 20 t  
 ORIGIN

Query Match 0.5%; Score 24; DB 6; Length 65;  
 Best Local Similarity 68.8%; Pred. No. 8e+05;  
 Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 2914 GGGTACATTTTGGATTGATGATCATTAAGAGTTGTCCTTGATG 2961  
 DB 2 GGTCAAAAGATTGAAGATGTATCTGAAGAAGTGTGATTTGGT 49

RESULT 21  
 LOCUS AX207310 66 bp DNA linear PAT 30-AUG-2001  
 DEFINITION Sequence 35 from Patent WO0155371.  
 ACCESSION AX207310  
 VERSION AX207310.1 GI:15395100  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE  
 AUTHORS Mauro, V.P., Edelman, G.M., Chappell, G.M., Jones, F.S., Owens, G. and Meech, R.  
 TITLE Methods of identifying synthetic transcriptional and translational regulatory elements, and compositions relating to same  
 JOURNAL Patent: WO 0155371-A 35 02-AUG-2001;  
 The Scripps Research Institute (US)  
 FEATURES  
 source 1..66  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="transcriptional regulatory element"  
 BASE COUNT 13 a 14 c 22 g 17 t  
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Query Match 0.5%; Score 24; DB 6; Length 66;  
 Best Local Similarity 60.9%; Pred. No. 8e+05;  
 Matches 39; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 4795 GTTCAAAAGAGTTGTAGCTGATCATGCGGCCATACCTGTTTAACTCCTGTTG 4854  
 DB 1 GATCAATTCAGAGAGGAGGATGCGAGCGACCGCTCGCTTCCGCTTATGTGTTG 60

OY 4855 TTGA 4858  
 DB 61 TGGA 64

RESULT 22  
 LOCUS AB04840511 88 bp DNA linear PRI 04-AUG-2001  
 DEFINITION Homo sapiens PDE11A gene, exon 11.  
 ACCESSION AB048411  
 VERSION AB048411.1 GI:15128469  
 KEYWORDS  
 SOURCE Homo sapiens DNA.  
 ORGANISM Homo sapiens; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
 AUTHORS Yuasa, K., Kanoh, Y., Okumura, K. and Omori, K.  
 TITLE Genomic organization and expression of the human phosphodiesterase PDE11A gene. Evolutionary relationship with other PDEs containing GAF domains  
 JOURNAL Eur. J. Biochem. 268 (1), 168-178 (2001)  
 MEDLINE 20570133  
 REFERENCES Yuasa, K. and Omori, K.  
 DIRECT SUBMISSION

## JOURNAL

Submitted (06-SEP-2000) Kenji Omori, Tanabe Seiyaku Co Ltd.,  
Discovery Research Laboratory: 2-50, Kawajishi-2-chome, Toda,  
Saitama 335-8505, Japan (E-mail: k-omori@tanabe.co.jp,  
Tel:81-48-433-8069, Fax:81-48-433-8159)

## FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="2"

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/gene="PDE11A"

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79..>88

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/number=11

28 a 14 c 22 g 24 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 24; DB 9; Length 88;

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QY 1760 AGTGAAGAGGCTCTGAGGCGCGCTGATGAAGACAGTACCTACCTGATGCTGC 1819

DB 21 AGTGTAAACAGACTGTGGGAAACCTTTGATGATGACATCAACGACTTTTGGAGGT 80

QY 1820 AGGA 1823

DB 81 AAGA 84

RESULT 23

AR014621

LOCUS

DEFINITION Sequence 63 from patent US 5773691.

ACCESSION AR014621

VERSION AR014621.1 GI:3972075

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 97)

Falco,S.Carli, Keeler,S.Jo. and Rice,J. Ann.

Chimeric genes and methods for increasing the lysine and threonine

content of the seeds of plants

Patent: US 5773691-A 63 30-JUN-1998;

Location/Qualifiers

1..97

/organism="unknown"

BASE COUNT 36 a 5 c 43 g 13 t

ORIGIN

Query Match

Best Local Similarity 0.5%; Score 24; DB 6; Length 97;

Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAGAGTGAAGAGTGAAG 1179

DB 10 GAAAGATGAAGCGATGAGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 69

QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

RESULT 24

BD010413

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 97)

Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

nutritional value of essential amino acids for improvement of the

Patent: US 5559223-A 54 24-SEP-1996;

Location/Qualifiers

1..97

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BASE COUNT 36 a 5 c 43 g 13 t

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DB 10 GAAAGATGAAGCGATGAGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 69

QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 5559223.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

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ORGANISM

REFERENCE

1 (bases 1 to 97)

Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

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Patent: US 5559223-A 54 24-SEP-1996;

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QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAGAGTGAAGAGTGAAG 1179

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QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

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LOCUS

DEFINITION Sequence 54 from patent US 5559223.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

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REFERENCE

1 (bases 1 to 97)

Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

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Patent: US 5559223-A 54 24-SEP-1996;

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BASE COUNT 36 a 5 c 43 g 13 t

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Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

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QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

RESULT 25

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LOCUS

DEFINITION Sequence 54 from patent US 5559223.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

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Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

nutritional value of essential amino acids for improvement of the

Patent: US 5559223-A 54 24-SEP-1996;

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BASE COUNT 36 a 5 c 43 g 13 t

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DB 10 GAAAGATGAAGCGATGAGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 69

QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

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LOCUS

DEFINITION Sequence 54 from patent US 5559223.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

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1 (bases 1 to 97)

Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

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Patent: US 5559223-A 54 24-SEP-1996;

Location/Qualifiers

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QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAGAGTGAAGAGTGAAG 1179

DB 10 GAAAGATGAAGCGATGAGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 69

QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

RESULT 25

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LOCUS

DEFINITION Sequence 54 from patent US 5559223.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 97)

Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

nutritional value of essential amino acids for improvement of the

Patent: US 5559223-A 54 24-SEP-1996;

Location/Qualifiers

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BASE COUNT 36 a 5 c 43 g 13 t

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QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAGAGTGAAGAGTGAAG 1179

DB 10 GAAAGATGAAGCGATGAGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 69

QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 5559223.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

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REFERENCE

1 (bases 1 to 97)

Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

nutritional value of essential amino acids for improvement of the

Patent: US 5559223-A 54 24-SEP-1996;

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BASE COUNT 36 a 5 c 43 g 13 t

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Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1120 GAGTATGAGGCTGATGACACAGAGGATTAAGAGAGTTGAAGAGTGAAGAGTGAAG 1179

DB 10 GAAAGATGAAGCGATGAGAGAGAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 69

QY 1180 AGTGAAGAAGAA 1191

DB 70 AGAGAAGATGAA 81

RESULT 25

126754

LOCUS

DEFINITION Sequence 54 from patent US 5559223.

ACCESSION 126754

VERSION 126754.1 GI:1606624

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 97)

Falco,S.C., Keeler,S.J. and Rice,J.A.

Synthetic storage proteins with defined structure containing

nutritional value of essential amino acids for improvement of the

Patent: US 5559223-A 54 24-SEP-1996;

Location/Qualifiers

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ORIGIN

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Best Local Similarity 0.5%; Score 24; DB 6; Length 97;

Matches 42; Conservative 0; M



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PAGES  
PUBLICATION DATE  
SOURCE

SULT 32  
 2152519  
 CDS  
 DEFINITION  
 CD11b-leukocyte integrin alpha chain [human, Genomic, 94 bp  
 segment 19 of 31].  
 REGION  
 S52191  
 S52191.1 GI:263036  
 WORDS  
 .  
 19 of 31  
 COMMENT  
 RCCE  
 ORGANISM  
 Homo sapiens.  
 Homo sapiens

REFERENCE  
1 (pages 1 to 94)  
Fleming, J.C., Pahl, H.L., Gonzalez, D.A., Smith, T.F. and Tenen, D.G.  
Structural analysis of the CD11b gene and phylogenetic analysis of

detection of binding reactions

JOURNAL Patent: US 5843767-A 4 01-DEC-1998;  
 FEATURES Location/Qualifiers  
 source 1..87  
 BASE COUNT 24 a 10 c 18 g 32 t 3 others  
 ORIGIN

Query Match 0.5%; Score 23.6; DB 6; Length 87;  
 Best Local Similarity 57.6%; Pred. No. 1e+06;  
 Matches 38; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

QY 3801 CAAGAACTGACAGCAATTAATATATCGAGGATCAACACCCCAATCTGCTTG 3860  
 Db 83 CATTCAAATYCTGAGTATATCATTTATAGCAAGGCAATCCWACCAACAACTTCTG 24  
 QY 3861 GTATTT 3866  
 Db 23 GAATTT 18

RESULT 36  
 HUMUT770A 88 bp DNA linear STS 29-DEC-1994  
 LOCUS Human STS UT770, 5' primer bind, sequence tagged site.  
 DEFINITION L31186  
 ACCESSION L31186  
 VERSION L31186.1 GI:605227  
 KEYWORDS STS; PCR primer; STS sequence: microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 88)  
 AUTHORS Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Robertson,M., Bradley,P., Elsnier,T., Tingey,A., Lalouel,J.-M. and White,R.  
 TITLE Genetic and physical mapping of simple sequence repeat containing unpublished (1994)  
 JOURNAL Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics  
 COMMENT 2160 Eccles Institute of Human Genetics  
 Salt Lake City, UT 84112  
 e-mail: stecorona.med.utah.edu  
 Primer A: GCGTGGTAATAGAGCAG  
 Primer B: CACATTTCCCTTACAC  
 End to label: Primer B  
 PCR Profile:  
 Initial Denaturation: 94C 300sec  
 Cycles Denaturation Annealing Extension  
 C 10 sec. 58 C 10 sec. 72 C 20 sec. 31 94  
 54 C 10 sec. 72 C 20 sec. Mg++: 3.00 mM  
 Gel: Acrylamide 7%, Formamide 32%, Urea 34%  
 Alleles: 4.

FEATURES  
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Query Match 0.5%; Score 23.6; DB 11; Length 88;  
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 Matches 41; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 476 TTGAACCTTACACCTTTGCTTAAGCTTACCTCAGTCTCAAGAAAGAGAGGAGC 535  
 Db 7 TTGCACCTCTACGCTGGGTAATAGACAGANTCAGTCAAAAAGAGAGAGAGAGAGA 66  
 QY 536 AAGAGAGACAGAAATA 553

Db 67 MAGANAGANAGANAGANA 84

RESULT 37  
 AX326603/c 98 bp DNA linear PAT 07-JAN-2002  
 LOCUS AX326603  
 DEFINITION Sequence 24 from Patent WO0192579.  
 ACCESSION AX326603  
 VERSION AX326603.1 GI:18097366  
 KEYWORDS human.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1  
 AUTHORS Wenz,H.M. and Schroth,G.P.  
 TITLE Methods for detecting target nucleic acids using coupled ligation and amplification  
 JOURNAL Patent: WO 0192579-A 24 06-DEC-2001;  
 PE Corporation (NY) (US)

FEATURES  
 source Location/Qualifiers  
 1..98  
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 /db\_xref="taxon:9606"  
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BASE COUNT 23 a 14 c 20 g 41 t  
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Query Match 0.5%; Score 23.6; DB 6; Length 98;  
 Best Local Similarity 53.2%; Pred. No. 1e+06;  
 Matches 50; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 4527 AATATTACATAAAGACTGTCGACAGACGATATAGCTTTTAACCTTCAAGACTG 4586  
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 QY 4587 AAGAGTCGACAGGTGCAAGAGCTCACTTCTCCTG 4620  
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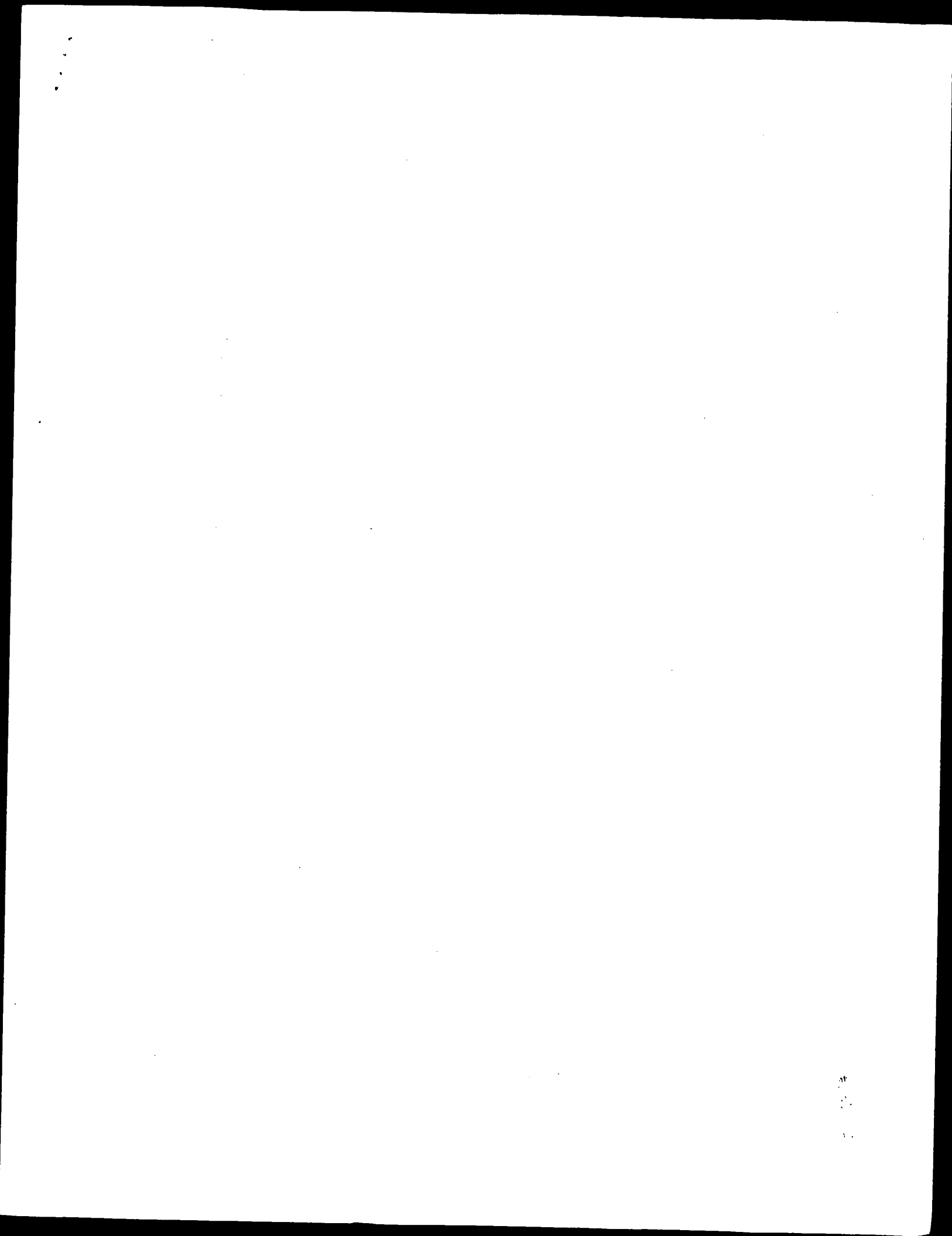
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 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 99)  
 AUTHORS Mijert,H.J., Stinder,L. and Kreutzmann,P.  
 TITLE Serin proteinase inhibitors  
 JOURNAL Patent: WO 0078963-A 10 28-DEC-2000;  
 FORSMANN, Wolf-Georg (DE)  
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 07:04:10 : Search time 109 Seconds  
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Title: US-09-676-436-3

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Scoring table: IDENTITY\_NUC  
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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 68418

Minimum DB seq length: 8

Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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C 8	24.6	0.5	71	4	US-08-973-124-78
C 9	24.6	0.5	71	5	PCT-US96-08014-78
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248	20.2	0.4	32	4	US-09-258-128-15	Sequence 15, Appl	321	20	0.4	60	5	US-08-362-2404-40	Sequence 40, Appl
249	20.2	0.4	65	3	US-08-445-463B-11	Sequence 11, Appl	322	20	0.4	62	4	PCT-US95-10245-40	Sequence 40, Appl
250	20.2	0.4	65	3	US-08-445-464C-11	Sequence 11, Appl	323	20	0.4	68	1	US-09-116-0332-34	Sequence 34, Appl
251	20.2	0.4	65	4	US-08-044-857D-11	Sequence 11, Appl	324	20	0.4	68	1	US-07-795-8599-13	Sequence 13, Appl
252	20.2	0.4	65	5	PCT-US94-03437-11	Sequence 11, Appl	325	20	0.4	68	1	US-08-457-616-13	Sequence 13, Appl
253	20.2	0.4	69	1	US-08-180-195-25	Sequence 25, Appl	326	20	0.4	70	4	US-09-446-0476-1	Sequence 1, Appl
254	20.2	0.4	69	1	US-08-434-001-78	Sequence 78, Appl	327	20	0.4	73	2	US-09-010-9288-8	Sequence 8, Appl
255	20.2	0.4	69	1	US-08-477-329-25	Sequence 25, Appl	328	20	0.4	74	4	US-09-305-008-8	Sequence 8, Appl
256	20.2	0.4	69	1	US-08-433-585-78	Sequence 78, Appl	329	20	0.4	75	1	US-08-195-874-5	Sequence 5, Appl
257	20.2	0.4	69	1	US-08-434-425-78	Sequence 78, Appl	330	20	0.4	75	1	PCT-US95-01671-5	Sequence 5, Appl
258	20.2	0.4	69	2	US-08-475-458-25	Sequence 25, Appl	331	20	0.4	81	2	US-08-451-472-54	Sequence 54, Appl
259	20.2	0.4	69	2	US-08-437-667-78	Sequence 78, Appl	332	20	0.4	81	2	US-08-469-537A-65	Sequence 65, Appl
260	20.2	0.4	69	3	US-08-906-955-78	Sequence 78, Appl	333	20	0.4	82	2	US-08-454-557C-81	Sequence 81, Appl
261	20.2	0.4	69	3	US-08-980-400-25	Sequence 25, Appl	334	20	0.4	82	2	US-08-340-446D-81	Sequence 81, Appl
262	20.2	0.4	69	3	US-08-945-909-78	Sequence 78, Appl	335	20	0.4	82	2	US-08-450-673C-81	Sequence 81, Appl
263	20.2	0.4	69	4	US-09-583-459A-25	Sequence 25, Appl	336	20	0.4	82	5	PCT-US95-17111A-81	Sequence 81, Appl
264	20.2	0.4	69	4	US-09-583-459A-25	Sequence 25, Appl	337	20	0.4	84	2	US-08-454-557C-91	Sequence 91, Appl
265	20.2	0.4	69	4	US-09-435-059-25	Sequence 25, Appl	338	20	0.4	84	2	US-08-340-446D-91	Sequence 91, Appl
266	20.2	0.4	69	4	US-09-396-002A-78	Sequence 78, Appl	339	20	0.4	84	5	US-08-450-673C-81	Sequence 81, Appl
267	20.2	0.4	69	5	PCT-US96-06060-78	Sequence 78, Appl	340	20	0.4	84	5	PCT-US95-10973A-36	Sequence 36, Appl
268	20.2	0.4	71	1	US-08-180-195-24	Sequence 24, Appl	341	20	0.4	88	1	US-07-964-624D-24	Sequence 24, Appl
269	20.2	0.4	71	1	US-08-477-329-24	Sequence 24, Appl	342	20	0.4	89	1	US-08-442-062-24	Sequence 24, Appl
270	20.2	0.4	71	2	US-08-475-458-24	Sequence 24, Appl	343	20	0.4	89	1	US-08-748-697A-24	Sequence 24, Appl
271	20.2	0.4	71	2	US-08-980-400-24	Sequence 24, Appl	344	20	0.4	89	4	US-09-165-616-24	Sequence 24, Appl
272	20.2	0.4	71	3	US-09-583-459A-24	Sequence 24, Appl	345	20	0.4	90	1	US-08-324-977-41	Sequence 41, Appl
273	20.2	0.4	71	3	US-09-583-459A-24	Sequence 24, Appl	346	20	0.4	90	2	US-08-384-616-41	Sequence 41, Appl
274	20.2	0.4	71	4	US-09-583-459A-24	Sequence 24, Appl	347	20	0.4	90	2	US-08-904-686A-41	Sequence 41, Appl
275	20.2	0.4	71	4	US-09-435-059-24	Sequence 24, Appl	348	20	0.4	90	4	US-09-115-850-41	Sequence 21, Appl
276	20.2	0.4	71	4	US-08-182-175A-30	Sequence 30, Appl	349	20	0.4	93	2	US-08-808-931-25	Sequence 21, Appl
277	20.2	0.4	84	1	US-08-474-633A-72	Sequence 72, Appl	350	20	0.4	93	3	US-08-808-931-25	Sequence 21, Appl
278	20.2	0.4	84	1	US-08-823-771-72	Sequence 72, Appl	351	20	0.4	93	3	US-09-050-603A-25	Sequence 21, Appl
279	20.2	0.4	84	2	PCT-US92-06412-30	Sequence 30, Appl	352	20	0.4	93	3	US-09-102-420B-25	Sequence 21, Appl
280	20.2	0.4	84	2	US-09-371-774-101	Sequence 101, Appl	353	20	0.4	93	4	US-08-706-945D-116	Sequence 16, Appl
281	20.2	0.4	87	2	US-08-763-106-44	Sequence 44, Appl	354	20	0.4	94	4	US-08-153-071-2	Sequence 2, Appl
282	20.2	0.4	87	2	US-09-320-774-44	Sequence 44, Appl	355	20	0.4	95	1	US-08-609-271-9	Sequence 9, Appl
283	20.2	0.4	90	4	US-09-461-697-375	Sequence 375, Appl	356	20	0.4	95	1	US-08-688-649-9	Sequence 9, Appl
284	20.2	0.4	90	4	US-08-479-783A-75	Sequence 75, Appl	357	20	0.4	95	2	US-08-438-511-2	Sequence 2, Appl
285	20.2	0.4	93	1	US-08-479-725-75	Sequence 75, Appl	358	20	0.4	95	2	US-08-188-374-9	Sequence 9, Appl
286	20.2	0.4	93	1	US-08-618-693-75	Sequence 75, Appl	359	20	0.4	95	3	US-08-973-629-5	Sequence 5, Appl
287	20.2	0.4	95	3	US-08-789-333F-96	Sequence 96, Appl	360	20	0.4	95	3	US-08-954-395A-28	Sequence 28, Appl
288	20.2	0.4	95	3	US-08-691-743C-75	Sequence 75, Appl	361	20	0.4	95	3	US-08-455-668E-47	Sequence 47, Appl
289	20.2	0.4	95	4	US-08-891-743C-75	Sequence 75, Appl	362	20	0.4	100	4	US-08-455-668E-47	Sequence 47, Appl
290	20.2	0.4	95	4	US-08-787-738B-96	Sequence 96, Appl	363	20	0.4	41	2	PCT-US91-03540A-2	Sequence 2, Appl
291	20.2	0.4	95	4	US-08-519-783A-157	Sequence 157, Appl	364	20	0.4	60	6	PCT-US91-03540A-2	Sequence 2, Appl
292	20.2	0.4	95	4	US-08-441-430-8	Sequence 8, Appl	365	20	0.4	60	6	PCT-US91-03540A-2	Sequence 2, Appl
293	20.2	0.4	95	5	PCT-US96-08014-164	Sequence 164, Appl	366	20	0.4	61	4	US-09-254-968-127	Sequence 127, Appl
294	20.2	0.4	96	1	US-08-088-658-42	Sequence 42, Appl	367	20	0.4	61	4	US-08-750-191A-4	Sequence 4, Appl
295	20.2	0.4	96	1	US-08-056-556-210	Sequence 210, Appl	368	20	0.4	63	3	US-08-457-274A-20	Sequence 20, Appl
296	20.2	0.4	98	2	US-09-072-596-205	Sequence 205, Appl	369	20	0.4	64	1	PCT-US95-05758-20	Sequence 20, Appl
297	20.2	0.4	98	2	US-08-471-907A-42	Sequence 42, Appl	370	20	0.4	64	1	US-08-374-641-6	Sequence 6, Appl
298	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	371	20	0.4	65	1	US-08-197-801-6	Sequence 6, Appl
299	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	372	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
300	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	373	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
301	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	374	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
302	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	375	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
303	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	376	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
304	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	377	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
305	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	378	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
306	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	379	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
307	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	380	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
308	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	381	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
309	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	382	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
310	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	383	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
311	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	384	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
312	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	385	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
313	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	386	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
314	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	387	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
315	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	388	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
316	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	389	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
317	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	390	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
318	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	391	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl
319	20.2	0.4	98	2	US-08-495-743-24	Sequence 24, Appl	392	20	0.4	65	1	US-09-197-801-6	Sequence 6, Appl

393	19.8	0.4	84	1	US-07-989-844-4	Sequence 4, Appl	C 466	19.6	0.4	78	2	US-08-478-373-124	Sequence 124, App
394	19.8	0.4	84	1	US-08-161-044-4	Sequence 4, Appl	C 467	19.6	0.4	78	3	US-08-474-671-124	Sequence 124, App
395	19.8	0.4	84	1	US-08-240-121-4	Sequence 4, Appl	C 468	19.6	0.4	78	3	US-08-483-577A-124	Sequence 124, App
396	19.8	0.4	84	1	US-08-451-241-4	Sequence 4, Appl	C 469	19.6	0.4	78	4	US-08-897-438-124	Sequence 124, App
397	19.8	0.4	84	5	PCT-US93-11297-4	Sequence 20, Appl	C 470	19.6	0.4	78	4	US-08-637-654-124	Sequence 124, App
398	19.8	0.4	84	5	PCT-US93-11298-20	Sequence 20, Appl	C 471	19.6	0.4	78	4	US-08-649-518-124	Sequence 124, App
399	19.8	0.4	86	1	US-09-206-942-2	Sequence 20, Appl	C 472	19.6	0.4	82	1	US-08-367-122-53	Sequence 53, Appl
400	19.8	0.4	86	1	US-08-477-877B-59	Sequence 59, Appl	C 473	19.6	0.4	86	4	US-08-464-700-21	Sequence 21, Appl
401	19.8	0.4	88	1	US-08-472-281A-59	Sequence 59, Appl	C 474	19.6	0.4	87	1	US-07-741-931-1	Sequence 1, Appl
402	19.8	0.4	88	2	US-08-477-989B-59	Sequence 59, Appl	C 475	19.6	0.4	87	1	US-08-937-132A-1	Sequence 1, Appl
403	19.8	0.4	88	2	US-09-208-966-30	Sequence 30, Appl	C 476	19.6	0.4	87	2	US-08-253-877C-63	Sequence 63, Appl
404	19.8	0.4	88	4	US-09-105-390-21	Sequence 21, Appl	C 477	19.6	0.4	87	2	US-08-452-164A-63	Sequence 63, Appl
405	19.8	0.4	90	1	US-08-252-057-21	Sequence 21, Appl	C 478	19.6	0.4	88	1	US-08-207-547A-1	Sequence 1, Appl
406	19.8	0.4	90	1	US-08-184-731-21	Sequence 21, Appl	C 479	19.6	0.4	88	2	US-08-702-652-1	Sequence 1, Appl
407	19.8	0.4	92	1	US-08-487-141B-109	Sequence 109, App	C 480	19.6	0.4	88	2	US-08-974-59A-672	Sequence 1, Appl
408	19.8	0.4	96	3	US-08-737-336-2	Sequence 2, Appl	C 481	19.6	0.4	90	4	US-08-556-978B-94	Sequence 94, Appl
409	19.8	0.4	96	3	US-08-484-322-3	Sequence 3, Appl	C 482	19.6	0.4	90	4	US-09-513-783A-129	Sequence 129, App
410	19.8	0.4	96	3	US-09-156-856-17	Sequence 17, Appl	C 483	19.6	0.4	90	4	US-08-556-978B-24	Sequence 24, Appl
411	19.8	0.4	98	5	PCT-US94-06456-19	Sequence 19, Appl	C 484	19.6	0.4	93	4	US-08-556-978B-25	Sequence 25, Appl
412	19.8	0.4	98	5	PCT-US94-06456-48	Sequence 48, Appl	C 485	19.6	0.4	94	4	US-09-125-642C-6	Sequence 6, Appl
413	19.8	0.4	99	4	US-09-244-794A-21	Sequence 21, Appl	C 486	19.6	0.4	94	4	US-08-479-783A-80	Sequence 80, Appl
414	19.8	0.4	99	4	US-09-007-005-21	Sequence 21, Appl	C 487	19.6	0.4	96	1	US-08-479-725-80	Sequence 80, Appl
415	19.8	0.4	99	4	US-09-247-190-21	Sequence 21, Appl	C 488	19.6	0.4	96	4	US-08-911-743C-80	Sequence 80, Appl
416	19.8	0.4	99	4	US-08-117-374-9	Sequence 9, Appl	C 489	19.6	0.4	96	4	US-08-991-743C-80	Sequence 80, Appl
417	19.8	0.4	53	1	US-08-280-263-9	Sequence 9, Appl	C 490	19.6	0.4	96	4	US-08-464-700-46	Sequence 80, Appl
418	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 491	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
419	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 492	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
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421	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 494	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
422	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 495	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
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456	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 529	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
457	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 530	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
458	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 531	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
459	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 532	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
460	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 533	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
461	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 534	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
462	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 535	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
463	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 536	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
464	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 537	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl
465	19.6	0.4	53	3	US-08-597-325-9	Sequence 9, Appl	C 538	19.6	0.4	96	4	US-08-479-725-80	Sequence 80, Appl

539	19.4	0.4	68	5	PCT-US96-06060-197	Sequence 197, App	C 612	19.2	0.4	45	4	US-09-414-117-76	Sequence 76, App
540	19.4	0.4	70	1	US-08-090-193-41	Sequence 41, App	C 613	19.2	0.4	45	4	US-09-678-437-76	Sequence 76, App
541	19.4	0.4	70	2	US-08-488-031-41	Sequence 41, App	C 614	19.2	0.4	47	4	US-09-438-016-2	Sequence 2, App
542	19.4	0.4	70	2	US-08-486-569-41	Sequence 41, App	C 615	19.2	0.4	47	4	US-09-438-016-8	Sequence 8, App
543	19.4	0.4	70	2	US-08-488-027-41	Sequence 41, App	C 616	19.2	0.4	48	1	US-07-797-556-9	Sequence 9, App
544	19.4	0.4	70	2	US-08-090-192-40	Sequence 40, App	C 617	19.2	0.4	49	1	US-09-538-709-1005	Sequence 1005, App
545	19.4	0.4	70	2	US-08-482-663-41	Sequence 41, App	C 618	19.2	0.4	54	1	US-08-758-306-952	Sequence 952, App
546	19.4	0.4	70	3	US-08-482-658-41	Sequence 41, App	C 619	19.2	0.4	54	2	US-08-585-684B-2660	Sequence 2660, App
547	19.4	0.4	70	3	US-08-470-349-40	Sequence 40, App	C 620	19.2	0.4	54	4	US-09-038-073-2660	Sequence 2660, App
548	19.4	0.4	70	3	US-08-618-1008-31	Sequence 31, App	C 621	19.2	0.4	55	4	US-09-383-143-6	Sequence 6, App
549	19.4	0.4	70	3	US-08-475-610-41	Sequence 41, App	C 622	19.2	0.4	55	4	US-09-394-630-4	Sequence 4, App
550	19.4	0.4	70	3	US-09-275-850-144	Sequence 144, App	C 623	19.2	0.4	58	3	US-08-718-904-103	Sequence 103, App
551	19.4	0.4	70	5	PCT-US92-00277-41	Sequence 41, App	C 624	19.2	0.4	62	4	US-08-464-514-22	Sequence 22, App
552	19.4	0.4	71	5	PCT-US92-00278-40	Sequence 40, App	C 625	19.2	0.4	62	4	US-08-486-403-22	Sequence 22, App
553	19.4	0.4	71	1	US-08-803-824-4	Sequence 4, App	C 626	19.2	0.4	69	2	US-08-894-578-166	Sequence 166, App
554	19.4	0.4	71	2	US-08-803-824-4	Sequence 4, App	C 627	19.2	0.4	71	2	US-08-465-591A-68	Sequence 68, App
555	19.4	0.4	71	2	US-09-057-937-4	Sequence 3, App	C 628	19.2	0.4	71	2	US-08-465-594A-68	Sequence 68, App
556	19.4	0.4	72	1	US-08-446-102-3	Sequence 3, App	C 629	19.2	0.4	71	4	US-08-973-124-283	Sequence 253, App
557	19.4	0.4	75	2	US-08-548-211-2	Sequence 2, App	C 630	19.2	0.4	71	5	PCT-US96-08014-253	Sequence 253, App
558	19.4	0.4	76	2	US-08-548-211-1	Sequence 1, App	C 631	19.2	0.4	72	1	US-08-433-126A-34	Sequence 34, App
559	19.4	0.4	78	1	US-07-927-316A-3	Sequence 3, App	C 632	19.2	0.4	72	1	US-08-976-413A-34	Sequence 34, App
560	19.4	0.4	78	1	US-08-459-263-6	Sequence 6, App	C 633	19.2	0.4	72	3	US-08-433-126A-34	Sequence 27, App
561	19.4	0.4	78	1	US-08-459-263-6	Sequence 6, App	C 634	19.2	0.4	72	3	US-09-476-299-27	Sequence 27, App
562	19.4	0.4	80	4	US-09-461-697-378	Sequence 378, App	C 635	19.2	0.4	72	4	US-09-609-134-27	Sequence 34, App
563	19.4	0.4	80	4	US-07-832-905B-61	Sequence 61, App	C 636	19.2	0.4	72	5	PCT-US96-06059-34	Sequence 34, App
564	19.4	0.4	80	2	US-07-832-905B-62	Sequence 62, App	C 637	19.2	0.4	73	1	US-08-434-001-61	Sequence 61, App
565	19.4	0.4	80	2	US-08-700-757-61	Sequence 61, App	C 638	19.2	0.4	73	1	US-08-433-585-61	Sequence 61, App
566	19.4	0.4	81	1	US-08-238-863-22	Sequence 22, App	C 639	19.2	0.4	73	1	US-08-433-585-61	Sequence 61, App
567	19.4	0.4	81	1	US-08-238-863-22	Sequence 22, App	C 640	19.2	0.4	73	1	US-08-434-425-61	Sequence 61, App
568	19.4	0.4	81	1	US-07-756-251A-14	Sequence 14, App	C 641	19.2	0.4	73	1	US-08-434-425-61	Sequence 61, App
569	19.4	0.4	81	1	US-08-443-407-22	Sequence 22, App	C 642	19.2	0.4	73	2	US-08-437-667-61	Sequence 61, App
570	19.4	0.4	81	1	US-08-443-407-22	Sequence 22, App	C 643	19.2	0.4	73	2	US-08-437-667-61	Sequence 61, App
571	19.4	0.4	81	1	US-08-443-407-22	Sequence 22, App	C 644	19.2	0.4	73	2	US-08-906-955-61	Sequence 61, App
572	19.4	0.4	81	5	PCT-US95-05600-166	Sequence 166, App	C 645	19.2	0.4	73	3	US-08-906-955-61	Sequence 61, App
573	19.4	0.4	81	5	PCT-US95-05600-166	Sequence 166, App	C 646	19.2	0.4	73	3	US-08-906-955-61	Sequence 61, App
574	19.4	0.4	82	1	US-08-497-134A-19	Sequence 19, App	C 647	19.2	0.4	73	3	US-08-945-909-61	Sequence 61, App
575	19.4	0.4	82	2	US-08-481-658B-37	Sequence 37, App	C 648	19.2	0.4	73	3	US-08-945-909-61	Sequence 61, App
576	19.4	0.4	82	2	US-08-477-504A-37	Sequence 37, App	C 649	19.2	0.4	73	4	US-09-396-002A-61	Sequence 61, App
577	19.4	0.4	82	2	US-08-486-756A-37	Sequence 37, App	C 650	19.2	0.4	73	4	US-09-396-002A-61	Sequence 61, App
578	19.4	0.4	82	2	US-08-485-862B-37	Sequence 37, App	C 651	19.2	0.4	73	5	PCT-US96-06060-61	Sequence 61, App
579	19.4	0.4	82	3	US-08-787-739-37	Sequence 37, App	C 652	19.2	0.4	73	5	PCT-US96-06060-61	Sequence 61, App
580	19.4	0.4	82	3	US-08-487-077A-37	Sequence 37, App	C 653	19.2	0.4	74	4	US-09-025-769B-154	Sequence 154, App
581	19.4	0.4	82	3	US-08-485-863A-37	Sequence 37, App	C 654	19.2	0.4	81	1	US-08-238-863-16	Sequence 16, App
582	19.4	0.4	82	4	US-08-485-863A-37	Sequence 37, App	C 655	19.2	0.4	81	1	US-08-443-407-16	Sequence 16, App
583	19.4	0.4	82	4	US-09-269-592-6	Sequence 6, App	C 656	19.2	0.4	81	1	US-08-443-407-16	Sequence 16, App
584	19.4	0.4	82	4	US-09-178-115-37	Sequence 37, App	C 657	19.2	0.4	81	1	US-08-447-169A-69	Sequence 69, App
585	19.4	0.4	82	4	US-09-177-776-37	Sequence 37, App	C 658	19.2	0.4	81	2	US-08-233-012C-69	Sequence 25, App
586	19.4	0.4	84	3	US-08-383-753-96	Sequence 96, App	C 659	19.2	0.4	83	3	PCT-US95-05600-160	Sequence 160, App
587	19.4	0.4	85	1	US-08-586-712-96	Sequence 96, App	C 660	19.2	0.4	83	3	US-08-783-853A-82	Sequence 82, App
588	19.4	0.4	85	2	US-08-959-512-96	Sequence 96, App	C 661	19.2	0.4	86	3	US-09-344-050-82	Sequence 82, App
589	19.4	0.4	85	2	US-09-512-983-96	Sequence 96, App	C 662	19.2	0.4	86	3	US-08-637-759B-1	Sequence 1, App
590	19.4	0.4	85	4	US-09-364-543-88	Sequence 88, App	C 663	19.2	0.4	89	2	US-08-637-759B-1	Sequence 1, App
591	19.4	0.4	87	3	US-08-836-561-90	Sequence 90, App	C 664	19.2	0.4	89	3	US-08-871-355A-1	Sequence 1, App
592	19.4	0.4	88	3	US-08-836-561-95	Sequence 95, App	C 665	19.2	0.4	89	4	US-08-887-534A-97	Sequence 97, App
593	19.4	0.4	88	3	US-07-964-624D-32	Sequence 32, App	C 666	19.2	0.4	89	4	US-08-836-561-84	Sequence 84, App
594	19.4	0.4	89	1	US-08-442-062-32	Sequence 32, App	C 667	19.2	0.4	90	2	US-08-356-361-24	Sequence 24, App
595	19.4	0.4	89	1	US-08-748-697A-32	Sequence 32, App	C 668	19.2	0.4	90	2	US-08-769-967A-74	Sequence 74, App
596	19.4	0.4	89	3	US-08-959-853-10	Sequence 10, App	C 669	19.2	0.4	90	2	US-08-974-549A-702	Sequence 702, App
597	19.4	0.4	89	3	US-09-165-616-32	Sequence 32, App	C 670	19.2	0.4	91	3	US-08-783-853A-82	Sequence 82, App
598	19.4	0.4	93	2	US-08-592-383-8	Sequence 8, App	C 671	19.2	0.4	91	3	US-09-344-050-16	Sequence 16, App
599	19.4	0.4	93	2	US-08-467-963C-34	Sequence 34, App	C 672	19.2	0.4	92	3	US-08-836-561-84	Sequence 84, App
600	19.4	0.4	98	2	US-08-838-189D-34	Sequence 34, App	C 673	19.2	0.4	93	2	US-08-836-561-84	Sequence 84, App
601	19.4	0.4	98	2	US-08-838-189D-34	Sequence 34, App	C 674	19.2	0.4	93	2	US-08-836-561-84	Sequence 84, App
602	19.4	0.4	98	3	US-08-344-639E-34	Sequence 34, App	C 675	19.2	0.4	97	1	US-08-305-699-17	Sequence 17, App
603	19.4	0.4	98	3	US-08-344-639E-34	Sequence 34, App	C 676	19.2	0.4	97	1	US-08-447-172A-34	Sequence 34, App
604	19.4	0.4	98	4	US-08-145-705A-16	Sequence 16, App	C 677	19.2	0.4	98	2	US-08-263-911-14	Sequence 14, App
605	19.4	0.4	100	3	US-08-836-561-84	Sequence 16, App	C 678	19.2	0.4	100	1	US-07-797-556-7	Sequence 7, App
606	19.4	0.4	100	3	US-09-269-592-16	Sequence 16, App	C 679	19.2	0.4	100	1	US-08-217-210B-7	Sequence 7, App
607	19.4	0.4	100	3	US-08-464-51A-19	Sequence 19, App	C 680	19.2	0.4	100	1	US-09-298-886-15	Sequence 15, App
608	19.2	0.4	34	4	US-08-486-403-19	Sequence 19, App	C 681	19.2	0.4	100	4	US-08-334-847-730	Sequence 730, App
609	19.2	0.4	34	4	US-08-830-04B-76	Sequence 76, App	C 682	19.2	0.4	36	1	US-08-010-633A-28	Sequence 28, App
610	19.2	0.4	45	2	US-08-050-47B-76	Sequence 76, App	C 683	19.2	0.4	42	3	US-08-805-631A-28	Sequence 28, App
611	19.2	0.4	45	2	US-08-050-47B-76	Sequence 76, App	C 684	19.2	0.4	42	3	US-08-805-631A-28	Sequence 28, App

C 685	19	0.4	42	4	US-09-569-344-28	Sequence 28, App1	C 758	19	0.4	71	4	US-09-364-902-27	Sequence 27, App1
C 686	19	0.4	47	2	US-08-621-803-244	Sequence 244, App	C 759	19	0.4	72	3	US-08-506-553-15	Sequence 15, App1
C 687	19	0.4	47	2	US-09-217-352-244	Sequence 244, App	C 760	19	0.4	73	1	US-08-567-047-7	Sequence 7, App1
C 688	19	0.4	48	1	US-08-317-102-2	Sequence 2, App1	C 761	19	0.4	73	1	US-08-567-047-8	Sequence 8, App1
C 689	19	0.4	49	4	US-08-706-945D-99	Sequence 99, App1	C 762	19	0.4	73	2	US-08-567-048-7	Sequence 7, App1
C 690	19	0.4	50	1	US-08-171-389-587	Sequence 587, App	C 763	19	0.4	73	2	US-08-567-048-8	Sequence 8, App1
C 691	19	0.4	50	1	US-08-123-936-587	Sequence 587, App	C 764	19	0.4	73	2	US-08-567-048-8	Sequence 8, App1
C 692	19	0.4	50	2	US-08-475-228A-587	Sequence 587, App	C 765	19	0.4	73	1	US-08-446-102-1	Sequence 1, App1
C 693	19	0.4	50	3	US-08-482-080A-587	Sequence 587, App	C 766	19	0.4	78	1	US-08-446-102-2	Sequence 2, App1
C 694	19	0.4	50	4	US-09-354-947-587	Sequence 587, App	C 767	19	0.4	78	1	US-08-446-169A-87	Sequence 87, App1
C 695	19	0.4	50	5	PCT-US93-12388-567	Sequence 587, App	C 768	19	0.4	78	2	US-08-233-012C-87	Sequence 87, App1
C 696	19	0.4	52	1	US-08-171-389-238	Sequence 238, App	C 769	19	0.4	78	4	US-08-617-010C-15	Sequence 15, App1
C 697	19	0.4	52	1	US-08-530-492-123	Sequence 123, App	C 770	19	0.4	78	4	US-09-566-591-15	Sequence 15, App1
C 698	19	0.4	52	2	US-08-123-936-238	Sequence 238, App	C 771	19	0.4	78	4	US-08-744-481A-25	Sequence 25, App1
C 699	19	0.4	52	2	US-08-475-228A-238	Sequence 238, App	C 772	19	0.4	79	4	US-08-839-624-8	Sequence 25, App1
C 700	19	0.4	52	3	US-08-482-080A-238	Sequence 238, App	C 773	19	0.4	79	4	US-08-839-624-8	Sequence 25, App1
C 701	19	0.4	52	4	US-08-906-517-123	Sequence 123, App	C 774	19	0.4	80	1	US-08-595-226B-4	Sequence 8, App1
C 702	19	0.4	52	4	US-09-143-634-27	Sequence 27, App1	C 775	19	0.4	80	2	US-08-906-491-4	Sequence 8, App1
C 703	19	0.4	52	4	US-09-354-947-238	Sequence 238, App	C 776	19	0.4	80	3	US-08-513-968-52	Sequence 52, App1
C 704	19	0.4	53	4	PCT-US93-12388-238	Sequence 238, App	C 777	19	0.4	80	3	US-08-513-968-52	Sequence 52, App1
C 705	19	0.4	53	4	US-09-091-814-28	Sequence 28, App1	C 778	19	0.4	80	3	US-08-513-968-52	Sequence 52, App1
C 706	19	0.4	54	4	US-09-091-814-28	Sequence 28, App1	C 779	19	0.4	80	4	US-08-506-553C-16	Sequence 16, App1
C 707	19	0.4	54	4	US-08-584-040-8241	Sequence 8241, App	C 780	19	0.4	80	4	US-09-188-214-4	Sequence 4, App1
C 708	19	0.4	57	1	US-08-741-881-81	Sequence 8241, App	C 781	19	0.4	80	4	US-09-188-214-4	Sequence 4, App1
C 709	19	0.4	57	1	US-08-739-158-81	Sequence 81, App1	C 782	19	0.4	80	4	US-09-149-727-59	Sequence 4, App1
C 710	19	0.4	57	2	US-08-739-158-81	Sequence 81, App1	C 783	19	0.4	81	4	US-08-839-624-8	Sequence 4, App1
C 711	19	0.4	57	2	US-08-596-387B-49	Sequence 49, App1	C 784	19	0.4	81	4	US-08-238-863-71	Sequence 71, App1
C 712	19	0.4	57	3	US-08-404-796-81	Sequence 81, App1	C 785	19	0.4	81	1	US-08-318-193-11	Sequence 31, App1
C 713	19	0.4	57	3	US-08-931-869-81	Sequence 81, App1	C 786	19	0.4	81	1	US-08-443-407-11	Sequence 11, App1
C 714	19	0.4	57	3	US-09-067-615-49	Sequence 49, App1	C 787	19	0.4	81	2	US-08-332-562A-10	Sequence 10, App1
C 715	19	0.4	57	4	US-09-350-399-81	Sequence 81, App1	C 788	19	0.4	81	4	US-08-839-624-8	Sequence 4, App1
C 716	19	0.4	57	4	US-09-350-399-81	Sequence 81, App1	C 789	19	0.4	81	4	US-08-556-928B-90	Sequence 90, App1
C 717	19	0.4	57	5	PCT-US95-09816A-49	Sequence 49, App1	C 790	19	0.4	81	4	US-08-470-953A-8	Sequence 32, App1
C 718	19	0.4	58	1	US-08-171-389-25	Sequence 25, App1	C 791	19	0.4	81	4	US-08-470-953A-8	Sequence 32, App1
C 719	19	0.4	58	1	US-08-123-936-25	Sequence 25, App1	C 792	19	0.4	81	5	PCT-US95-05600-215	Sequence 25, App1
C 720	19	0.4	58	1	US-08-625-691-31	Sequence 31, App1	C 793	19	0.4	82	6	US-09-149-727-71	Sequence 71, App1
C 721	19	0.4	58	2	US-08-475-228A-25	Sequence 25, App1	C 794	19	0.4	82	6	US-08-976-613A-253	Sequence 253, App1
C 722	19	0.4	58	3	US-08-482-080A-25	Sequence 25, App1	C 795	19	0.4	83	3	US-07-964-624D-45	Sequence 45, App1
C 723	19	0.4	58	4	US-09-387-699-16	Sequence 16, App1	C 796	19	0.4	84	1	US-08-442-062-45	Sequence 45, App1
C 724	19	0.4	58	4	US-09-140-201-6	Sequence 6, App1	C 797	19	0.4	84	1	US-08-442-062-45	Sequence 45, App1
C 725	19	0.4	58	4	US-09-354-947-25	Sequence 25, App1	C 798	19	0.4	84	1	US-08-748-697A-45	Sequence 45, App1
C 726	19	0.4	58	4	US-09-641-259B-16	Sequence 16, App1	C 799	19	0.4	85	4	US-09-165-616-45	Sequence 45, App1
C 727	19	0.4	58	4	PCT-US93-06751-132	Sequence 132, App	C 800	19	0.4	85	4	US-08-839-624-31	Sequence 31, App1
C 728	19	0.4	58	5	PCT-US93-12388-25	Sequence 25, App1	C 801	19	0.4	85	4	US-08-839-624-31	Sequence 31, App1
C 729	19	0.4	60	4	US-09-116-032-16	Sequence 16, App1	C 802	19	0.4	86	1	US-07-630-288A-40	Sequence 40, App1
C 730	19	0.4	60	4	US-09-626-929-14	Sequence 14, App1	C 803	19	0.4	86	1	US-08-468-049-40	Sequence 40, App1
C 731	19	0.4	60	4	US-09-484-850-14	Sequence 14, App1	C 804	19	0.4	86	2	US-08-467-963C-11	Sequence 11, App1
C 732	19	0.4	60	4	US-09-408-392-14	Sequence 14, App1	C 805	19	0.4	86	2	US-08-852-344D-11	Sequence 11, App1
C 733	19	0.4	60	4	US-09-626-930-14	Sequence 14, App1	C 806	19	0.4	86	3	US-08-852-344D-11	Sequence 11, App1
C 734	19	0.4	60	4	US-09-626-930-14	Sequence 14, App1	C 807	19	0.4	86	3	US-08-467-963A-11	Sequence 11, App1
C 735	19	0.4	61	4	US-08-207-547A-17	Sequence 17, App1	C 808	19	0.4	86	4	US-08-467-963A-11	Sequence 11, App1
C 736	19	0.4	61	1	US-08-207-547A-26	Sequence 26, App1	C 809	19	0.4	86	4	US-08-467-963A-11	Sequence 11, App1
C 737	19	0.4	61	1	US-08-207-547A-26	Sequence 26, App1	C 810	19	0.4	86	4	US-08-467-963A-11	Sequence 11, App1
C 738	19	0.4	61	1	US-08-207-547A-26	Sequence 26, App1	C 811	19	0.4	87	1	US-08-433-126A-72	Sequence 72, App1
C 739	19	0.4	61	1	US-08-207-547A-26	Sequence 26, App1	C 812	19	0.4	87	1	US-08-433-126A-72	Sequence 72, App1
C 740	19	0.4	61	1	US-08-207-547A-26	Sequence 26, App1	C 813	19	0.4	87	1	US-08-433-126A-72	Sequence 72, App1
C 741	19	0.4	61	1	US-08-207-547A-26	Sequence 26, App1	C 814	19	0.4	87	1	US-08-433-126A-72	Sequence 72, App1
C 742	19	0.4	61	1	US-08-215-082-17	Sequence 17, App1	C 815	19	0.4	87	1	US-08-433-126A-72	Sequence 72, App1
C 743	19	0.4	61	1	US-08-215-082-17	Sequence 17, App1	C 816	19	0.4	87	1	US-08-433-126A-72	Sequence 72, App1
C 744	19	0.4	61	2	US-08-702-652-25	Sequence 25, App1	C 817	19	0.4	87	3	US-08-976-413A-72	Sequence 72, App1
C 745	19	0.4	61	2	US-08-702-652-25	Sequence 25, App1	C 818	19	0.4	87	3	US-08-976-413A-72	Sequence 72, App1
C 746	19	0.4	61	2	US-08-702-652-25	Sequence 25, App1	C 819	19	0.4	87	3	US-08-976-413A-72	Sequence 72, App1
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C 750	19	0.4	69	4	US-09-348-578-37	Sequence 37, App1	C 823	19	0.4	87	6	PCT-US96-06059-147	Sequence 147, App1
C 751	19	0.4	69	4	US-09-348-578-37	Sequence 37, App1	C 824	19	0.4	88	2	US-08-477-527A-203	Sequence 203, App1
C 752	19	0.4	70	1	US-08-487-141B-107	Sequence 107, App	C 825	19	0.4	88	3	US-08-836-561-90	Sequence 90, App1
C 753	19	0.4	70	2	US-08-927-561-107	Sequence 107, App	C 826	19	0.4	88	3	US-08-836-561-95	Sequence 95, App1
C 754	19	0.4	70	4	US-09-459-427-16	Sequence 16, App1	C 827	19	0.4	88	3	US-08-836-561-95	Sequence 95, App1
C 755	19	0.4	70	4	US-09-459-427-16	Sequence 16, App1	C 828	19	0.4	88	5	PCT-US96-09537-203	Sequence 203, App1
C 756	19	0.4	70	5	PCT-US96-09388-107	Sequence 107, App	C 829	19	0.4	88	5	PCT-US96-09537-203	Sequence 203, App1
C 757	19	0.4	71	4	US-09-237-712-40	Sequence 40, App1	C 830	19	0.4	90	1	US-08-383-761-2	Sequence 2, App1

831	19	0.4	90	1	US-08-824-277-2	Sequence 2, Appl	C 904	18.8	0.4	71	4	US-08-952-793-325	Sequence 325, App
832	19	0.4	90	2	US-08-762-106-44	Sequence 40, Appl	C 905	18.8	0.4	71	5	PCT-US96-094556-375	Sequence 325, App
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837	19	0.4	93	3	US-08-976-413A-407	Sequence 407, App	C 910	18.8	0.4	73	3	US-08-466-047B-9	Sequence 9, Appl
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839	19	0.4	93	4	US-08-330-535A-26	Sequence 26, Appl	C 912	18.8	0.4	74	4	US-09-315-794-33	Sequence 53, Appl
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841	19	0.4	94	2	US-08-838-844-26	Sequence 26, Appl	C 914	18.8	0.4	74	4	US-09-315-794-33	Sequence 53, Appl
842	19	0.4	94	4	US-08-905-223-124	Sequence 124, App	C 915	18.8	0.4	75	3	US-09-023-082A-118	Sequence 118, App
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845	19	0.4	95	1	US-08-468-049-39	Sequence 39, Appl	C 918	18.8	0.4	77	4	US-08-588-983-24	Sequence 24, Appl
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847	19	0.4	95	1	US-09-308-759A-41	Sequence 41, Appl	C 920	18.8	0.4	78	3	US-08-817-335-2	Sequence 2, Appl
848	19	0.4	95	1	US-09-308-759A-42	Sequence 42, Appl	C 921	18.8	0.4	78	3	US-08-817-335-2	Sequence 2, Appl
849	19	0.4	96	3	US-08-464-700-5	Sequence 58, Appl	C 922	18.8	0.4	78	4	US-09-025-769B-125	Sequence 125, App
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851	18.8	0.4	33	1	US-08-338-970B-24	Sequence 24, Appl	C 924	18.8	0.4	79	6	US-09-506-729-20	Sequence 20, Appl
852	18.8	0.4	33	1	US-08-401-908-11	Sequence 11, Appl	C 925	18.8	0.4	79	6	US-09-506-729-20	Sequence 20, Appl
853	18.8	0.4	33	3	US-08-814-412-29	Sequence 29, Appl	C 926	18.8	0.4	80	1	US-07-920-281C-25	Sequence 25, Appl
854	18.8	0.4	36	1	US-07-854-386B-29	Sequence 29, Appl	C 927	18.8	0.4	80	3	US-09-023-082A-33	Sequence 25, Appl
855	18.8	0.4	37	1	US-08-612-885A-7	Sequence 7, Appl	C 928	18.8	0.4	80	4	US-08-466-277-25	Sequence 25, Appl
856	18.8	0.4	37	3	US-09-093-293-7	Sequence 7, Appl	C 929	18.8	0.4	80	4	US-08-894-818B-38	Sequence 38, Appl
857	18.8	0.4	37	3	US-09-093-293-7	Sequence 7, Appl	C 930	18.8	0.4	81	4	US-09-157-748-43	Sequence 43, Appl
858	18.8	0.4	39	2	PCT-US94-10562A-7	Sequence 7, Appl	C 931	18.8	0.4	81	4	US-08-729-601A-33	Sequence 33, Appl
859	18.8	0.4	39	2	US-08-910-731-14	Sequence 14, Appl	C 932	18.8	0.4	83	4	US-09-603-663-39	Sequence 39, Appl
860	18.8	0.4	40	2	US-08-713-815A-6	Sequence 6, Appl	C 933	18.8	0.4	83	4	US-09-603-663-39	Sequence 39, Appl
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862	18.8	0.4	46	1	US-07-741-940-26	Sequence 26, Appl	C 935	18.8	0.4	84	1	US-08-687-080-58	Sequence 3, Appl
863	18.8	0.4	46	1	US-08-452-654-26	Sequence 26, Appl	C 936	18.8	0.4	84	1	US-08-687-080-58	Sequence 3, Appl
864	18.8	0.4	46	1	US-08-452-654-26	Sequence 26, Appl	C 937	18.8	0.4	84	1	US-08-687-080-58	Sequence 3, Appl
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866	18.8	0.4	46	3	US-08-450-582-26	Sequence 26, Appl	C 939	18.8	0.4	85	1	US-08-477-509E-68	Sequence 68, Appl
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870	18.8	0.4	47	4	US-09-641-638-1228	Sequence 1228, App	C 943	18.8	0.4	85	4	US-09-012-097A-54	Sequence 54, Appl
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881	18.8	0.4	54	1	US-08-390-950-1107	Sequence 1107, App	C 954	18.8	0.4	87	2	US-08-477-527A-200	Sequence 200, App
882	18.8	0.4	55	4	US-09-609-816-15	Sequence 15, Appl	C 955	18.8	0.4	87	3	PCT-US96-09537-200	Sequence 200, App
883	18.8	0.4	57	1	US-08-383-753-101	Sequence 101, App	C 956	18.8	0.4	88	3	US-08-481-710-200	Sequence 200, App
884	18.8	0.4	57	2	US-08-383-753-101	Sequence 101, App	C 957	18.8	0.4	88	3	PCT-US96-09537-200	Sequence 200, App
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C 979 18.8 0.4 91 3 US-08-839-765-140  
C 980 18.8 0.4 91 3 US-09-136-389-140  
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C 982 18.8 0.4 91 4 US-09-345-882-9  
C 983 18.8 0.4 92 5 PCT-US93-06251-39  
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C 985 18.8 0.4 95 1 US-08-105-483-376  
C 986 18.8 0.4 95 1 US-08-709-209-376  
C 987 18.8 0.4 95 1 US-08-458-101-376  
C 988 18.8 0.4 96 3 US-09-069-886-12  
C 989 18.8 0.4 97 3 US-08-434-099A-1  
C 990 18.8 0.4 97 3 US-08-825-852-43  
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## ALIGNMENTS

Sequence 140, App  
Sequence 41, App  
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Sequence 46, App  
Sequence 57, App  
Sequence 91, App

RESULT 1  
US-08-400-256-4/C  
Sequence 4, Application US/08400256  
Patent No. 5750497

## GENERAL INFORMATION:

APPLICANT: Havelund, Svend  
APPLICANT: Halstrom, John  
APPLICANT: Jonassen, Ib  
APPLICANT: Andersen, Asger Sloth  
TITLE OF INVENTION: ACYLATED INSULIN  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:

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CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/400,256  
FILING DATE: 03-MAR-1995

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J.  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 3985,220-US  
TELECOMMUNICATION INFORMATION:  
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INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-400-256-4

Query Match 0.5%; Score 26; DB 1; Length 100;  
Best Local Similarity 55.6%; Pred. No. 7.6e+02;  
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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DB 97 AAGCTGACGACGCTAAGGATATGATGAAACATGTGTACTTATCTGTCTTGTAC 38

QY 4529 TATTACATTAAGACTGTCTGAGACGAG 4558  
DB 37 CAATTGAAACTACTGTCTTACGACGAG 8

RESULT 2  
US-08-975-365-4/C  
Sequence 4, Application US/08975365  
Patent No. 6011007

## GENERAL INFORMATION:

APPLICANT: Havelund, Svend  
APPLICANT: Halstrom, John  
APPLICANT: Jonassen, Ib  
APPLICANT: Andersen, Asger Sloth  
TITLE OF INVENTION: ACYLATED INSULIN  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:

ADDRESS: No. 60110070 No. 6011007disk of No. 6011007th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/975,365  
FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/400,256  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J.  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 3985,220-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 100 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-975-365-4

Query Match 0.5%; Score 26; DB 3; Length 100;  
Best Local Similarity 55.6%; Pred. No. 7.6e+02;  
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 4469 AAGATGAAGCCCTAGTAAATATGACTTGAATATCTCTTAATCACTAGTATGTA 4528  
DB 97 AAGCTGACGACGCTAAGGATATGATGAAACATGTGTACTTATCTGTCTTGTAC 38

QY 4529 TATTACATTAAGACTGTCTGAGACGAG 4558  
DB 37 CAATTGAAACTACTGTCTTACGACGAG 8



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RESULT 3
US-08-427-097-5
; Sequence 5, Application US/08427097
; Patent No. 5668294
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Sommers, Anne O.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,097
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Feibert, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 40-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Oligonucleotide"
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-427-097-5

Query Match
Best Local Similarity 54.3%; Score 25.2; DB 1; Length 99;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3026 ATGTCTGACTAATGAGTGTAGAGGTACAGACCCAGGTGGCGACTCAAGCAT 3085
DB 2 AAGACCCAGCTATAGTGAAGCTGTACTGCTGCTATTCGATGGAAGCATGAGTGC 61
QY 3086 TTGATTTTCTACAGCAATTGACCTGCTTTAT 3119
DB 62 GTGAGCATACTCAGACCAAGCCAGTTGCTATAT 95

RESULT 4
US-08-878-957-5
; Sequence 5, Application US/08878957
; Patent No. 5965796
; GENERAL INFORMATION:
; APPLICANT: Meagher, Richard B.
; APPLICANT: Sommers, Anne O.
; TITLE OF INVENTION: Metal Resistance Sequences and
; TITLE OF INVENTION: Transgenic Plants
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
```

```
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,957
FILING DATE: 19-JUN-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/427,097
FILING DATE: 21-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Feibert, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 40-94A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-878-957-5

Query Match
Best Local Similarity 54.3%; Score 25.2; DB 2; Length 99;
Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3026 ATGTCTGACTAATGAGTGTAGAGGTACAGACCCAGGTGGCGACTCAAGCAT 3085
DB 2 AAGACCCAGCTATAGTGAAGCTGTACTGCTGCTATTCGATGGAAGCATGAGTGC 61
QY 3086 TTGATTTTCTACAGCAATTGACCTGCTTTAT 3119
DB 62 GTGAGCATACTCAGACCAAGCCAGTTGCTATAT 95

RESULT 5
US-09-641-638-918/c
; Sequence 918, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bouquellet, Lydie
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 918
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LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-458-424B-78

Query Match	0.5%;	Score 24.6;	DB 1;	Length 71;
Best Local Similarity	65.5%;	Pred. No. 1.5e+03;		
Matches 36;	Conservative 0;	Mismatches 19;	Indels 0;	Cane 0;

Wed Nov 13 14:22:41 2002

us-09-676-436-3.liml.rn1

Page 11

OY 3958 GAACATGCTAGTCTATTCACAGACATGCGATGCGATCCTCC 4012  
DB 56 GAAGACGTAACTAGTATTAAACATACCCCGCTGGCGCATGCTCTCC 2

RESULT 8  
US-08-973-124-78/c  
Sequence 78, Application US/08973124  
Patent No. 6207816  
GENERAL INFORMATION:  
APPLICANT: LARRY GOLD et al.  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
TITLE OF INVENTION: LIGANDS TO GROWTH  
TITLE OF INVENTION: FACTORS  
NUMBER OF SEQUENCES: 304  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,124  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08014  
FILING DATE: 30-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/459,423  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,424  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,594  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,591  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,725  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,783  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/618,693  
FILING DATE: 20-MARCH-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-973-124-78

Query Match 0.5%; Score 24.6; DB 4; Length 71;

Best Local Similarity 65.5%; Pred. No. 1.5e+03;  
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
OY 3958 GAACATGCTAGTCTATTCACAGACATGCGATGCGATCCTCC 4012  
DB 56 GAAGACGTAACTAGTATTAAACATACCCCGCTGGCGCATGCTCTCC 2

RESULT 9  
PCT-US96-08014-78/c  
Sequence 78, Application PC/TUS9608014  
GENERAL INFORMATION:  
APPLICANT: LARRY GOLD; NEROJA JANJIC; STEVEN RINGQUIST; NIKOS  
TITLE OF INVENTION: PENELOPE J. TOOTHMAN  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH  
TITLE OF INVENTION: FACTOR (TGF- $\beta$ ) PLATELET-DERIVED  
TITLE OF INVENTION: GROWTH FACTOR (PGCF) AND HUMAN  
NUMBER OF SEQUENCES: 304  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08014  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,423  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,424  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,594  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,591  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,725  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,783  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/618,693  
FILING DATE: 20-MARCH-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 78:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
PCT-US96-08014-78

Query Match 0.5%; Score 24.6; DB 5; Length 71;  
Best Local Similarity 65.5%; Pred. No. 1.5e+03;  
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 3958 GAACATGATAGTATGCTATATCAACACATCCATTCGATCAAGTCTCC 4012  
DB 56 GAACACGTAAGTATAGTATTAACACATCCATTCGATCAAGTCTCC 2

## RESULT 10

US-09-100-664A-5  
Sequence 5, Application US/09100664A  
Patent No. 6057129

## GENERAL INFORMATION:

APPLICANT: YOUNG, MICHAEL W.  
APPLICANT: KLOSS, BRIAN  
APPLICANT: BLAU, JUSTIN  
APPLICANT: PRICE, JEFFREY  
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,664A  
FILING DATE: 19-JUN-1998  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
TELEX: 133521

## INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 72 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULAR TYPE: CDNA  
HYPOTHEetical: NO  
US-09-100-664A-5

Query Match 0.5%; Score 24.6; DB 3; Length 72;  
Best Local Similarity 59.2%; Pred. No. 1.6e+03;  
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 3694 ATTGGAAGAGCCAGTATGGAAGGTGTACACCTGCATCACCGCGGAGACTG 3753  
DB 1 ATAGGATCGGATCGTTCGGGACATCTAAGTGGGACACGATCAACACTGGGAGAG 60  
OY 3754 ATGGCCATGAA 3764  
DB 61 GTGGCATCAA 71

## RESULT 11

US-09-335-983-5  
Sequence 5, Application US/09335983  
Patent No. 6436628  
GENERAL INFORMATION:

APPLICANT: Young, Michael W  
APPLICANT: Kloss, Brian  
APPLICANT: Blau, Justin  
APPLICANT: Price, Jeffrey

TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE THEREOF  
FILE REFERENCE: 600-1-221N  
CURRENT APPLICATION NUMBER: US/09/335,983  
EARLIER FILING DATE: 1999-06-18  
EARLIER APPLICATION NUMBER: 09/100,664  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 5

LENGTH: 72  
TYPE: DNA

ORGANISM: Drosophila melanogaster  
US-09-335-983-5

Query Match 0.5%; Score 24.6; DB 4; Length 72;  
Best Local Similarity 59.2%; Pred. No. 1.6e+03;  
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 3694 ATTGGAAGAGCCAGTATGGAAGGTGTACACCTGCATCACCGCGGAGACTG 3753  
DB 1 ATAGGATCGGATCGTTCGGGACATCTAAGTGGGACACGATCAACACTGGGAGAG 60  
OY 3754 ATGGCCATGAA 3764  
DB 61 GTGGCATCAA 71

## RESULT 12

US-09-506-729-21/c  
Sequence 21, Application US/09506729  
Patent No. 6365352

## GENERAL INFORMATION:

APPLICANT: Yerramilli, Subrahmanyam V.  
APPLICANT: Prashar, Yatindra  
APPLICANT: Newberger, Peter  
APPLICANT: Goguen, Jon  
TITLE OF INVENTION: A PROCESS TO STUDY CHANGES IN GENE EXPRESSION IN  
FILE REFERENCE: 44921-5016-US  
CURRENT APPLICATION NUMBER: US/09/506,729  
EARLIER FILING DATE: 2000-02-18  
EARLIER APPLICATION NUMBER: PCT/US98/17284  
EARLIER FILING DATE: 1998-08-21  
EARLIER APPLICATION NUMBER: 60/056,844  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 21  
LENGTH: 98  
TYPE: DNA

ORGANISM: Homo sapiens  
US-09-506-729-21

Query Match 0.5%; Score 24.6; DB 4; Length 98;  
Best Local Similarity 59.2%; Pred. No. 1.9e+03;  
Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

OY 4911 GTTGTATGCAAAAGCGTGTACTGTAATTAAGAAAAAGGCTCTTTTCAATTAAT 4970  
DB 93 GTTATCATACATAAGACCGCATGATATATACAAAGGGGGTCTTTTTCATTAAAC 34  
OY 4971 GGTATATTTTA 4981  
DB 33 GTTACAAATATA 23

## RESULT 13

US-08-400-256-9/c

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ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,365
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/400,256
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lambirth, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3985.220-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-975-365-9

Query Match
Best Local Similarity 0.5%; Score 24.4; DB 3; Length 100;
Matches 49; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

OY 4469 AAGAAATGGAAGCTTACTAGAAATATGACCTTGGAAAAATTCCTTAATCACTACTATGTAA 4528
DB 97 AAGTCGACGACGCGTAAGGCGATCGTTGACAAAGTGTGACTTCTATCTGTCTTTTATAC 38
OY 4529 TATTTACATTAAGACTGCTGCAAGACGAG 4558
DB 37 CAATTGGAAACTACTGTGTGTTAGACGCGAG 8

RESULT 15
US-08-182-175A-54
; Sequence 54, Application US/08182175A
; Patent No. 5559223
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,175A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743,006
; FILING DATE: 9 August 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Linda Axamelly Floyd

```



Wed Nov 13 14:22:41 2002

us-09-676-436-3.limit.ini

Page 15

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ATTORNEY/AGENT INFORMATION:
NAME: BARBARA C. STEGELL
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB-1037-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
FEATURE:
NAME/KEY: CDS /function= "synthetic
LOCATION: 2..88 /product= "protein"
OTHER INFORMATION:
storage protein
/sequence= "asp"
/standard_name=
"5.11.11.5"
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-08-823-771-63
Query Match 0.5%: Score 24; DB 4; Length 97;
Best Local Similarity 58.3%; Pred. No. 2.7e+03;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1120 GAGTATGAGGCTGATGACACAGAGAGATTAAGGAGCTTGAGAGAGTACGATGAG 1179
DB 10 GAAGATGAGGCGATGAGAGAGATGAGTGTGAGAGAGAGATGAGTGTGAGAGAGATGAGTGTGAG 69
QY 1180 AGTGAAGAGAA 1191
DB 70 AGAGAGAGATGAA 81
RESULT 18
PCT-US92-06412-54
; Sequence 54, Application PC/TUS9206412
; GENERAL INFORMATION:
; APPLICANT: Saverio Carl Falco
; APPLICANT: Sharon J. Keeler
; TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing F
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh System, 6.0
; SOFTWARE: Microsoft Word, 4.0
; CURRENT APPLICATION DATA: PCT/US92/06412
; APPLICATION NUMBER: 530
; FILING DATE: 19920807
; CLASSIFICATION: 530
; PRIORITY APPLICATION DATA: 07/743,006
; APPLICATION NUMBER: 9 August 1991
; FILING DATE: 9 August 1991
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```
ATTORNEY/AGENT INFORMATION:
NAME: Linda Axamethy Floyd
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BB-1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-4929
TELEFAX: (302) 892-7949
TELEX: 835420
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: E. coli
CELL TYPE: DH5 alpha
IMMEDIATE SOURCE:
CLONE: 92-2
FEATURE:
NAME/KEY: CDS /function= "synthetic storage protein
LOCATION: 2..88 /product= "protein"
OTHER INFORMATION:
storage protein
/sequence= "asp"
/standard_name= "5.11.11.5"
PCT-US92-06412-54
Query Match 0.5%: Score 24; DB 5; Length 97;
Best Local Similarity 58.3%; Pred. No. 2.7e+03;
Matches 42; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 1120 GAGTATGAGGCTGATGACACAGAGAGATTAAGGAGCTTGAGAGAGTACGATGAG 1179
DB 10 GAAGATGAGGCGATGAGAGAGATGAGTGTGAGAGAGAGATGAGTGTGAGAGAGATGAGTGTGAG 69
QY 1180 AGTGAAGAGAA 1191
DB 70 AGAGAGAGATGAA 81
RESULT 19
US-08-672-158A-8
; Sequence 8, Application US/08672158A
; Patent No. 5770371
; GENERAL INFORMATION:
; APPLICANT: Sheryl Thompson
; TITLE OF INVENTION: Modification of Cryptic Splice Sites In
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,158A
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis D., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4855,000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
```

FILE REFERENCE: GENSET.051CP1



Query Match	0.5%	Score 23	DB 3	length 60
Best Local	Similarity 68.1%	Pred No. 4e+03		
Matches 32	Conservative	0	Mismatches 15	Indels 0
				Gaps 0

NAME: Coruzzi, Laura A.

ORGANISM: *homo sapiens*  
INDIVIDUAL ISOLATE: SW1  
US-08-484-322-5

2598 TGTTCACACCCCTAGACAGCATGCAGGTGGATTAATCTTTACTAGTTGTCATGCAGTCTGC 265  
 77 TGTTCACACCATTAATATGCTGCTGCTCTCGGCTCTAGCTTTCGTCGCCGTTGGT 18  
 2658 G 2658  
 17 G 17

## RESULT 28

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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-766A-41

Query Match          0.4%; Score 22.4; DB 2; Length 95;
Best Local Similarity 55.0%; Pred. No. 7.6e+03;
Matches 44; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY   139 AAGGAAAAATGATGCACCAATCATCGCTCCACATAAAGACTGTGAAGAAAACAGTGGAG 198
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   1    AAGGAAAGGAAAGAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAGA 60
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   61 GAGGTGAAAAAAAAACAACACTA 80

RESULT 30
US-08-182-175A-48
Sequence 48, Application US/08182175A
Patent No. 5559223
GENERAL INFORMATION:
APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,175A
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/743,006
FILING DATE: 9 August 1991
ATTORNEY/AGENT INFORMATION:

```

RESULT 31  
US-08-474-633A-57  
Sequence 57, Application US/08474633A  
Patent No. 5773691  
GENERAL INFORMATION:  
APPLICANT: E. I. DU PONT DE NEMOURS AND  
APPLICANT: COMPANY  
TITLE OF INVENTION: CHIMERIC GENES AND  
METHODS FOR INCREASING  
TITLE OF INVENTION: INCREASING THE LYSINE  
TITLE OF INVENTION: AND THEORININE CONTENT  
TITLE OF INVENTION: OF THE SEEDS OF PLANTS  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS  
ADDRESS: AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: U.S.A.  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MICROSOFT WORD VERSION 2.0C  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,633A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIEGELL

RESULT 32  
 US-08-823-771-57  
 : Sequence 57, Application US/08823771  
 Patent No. 6459019  
 GENERAL INFORMATION:  
 APPLICANT: E. I. DU PONT DE NEMOURS AND  
 COMPANY  
 TITLE OF INVENTION: CHIMERIC GENES AND  
 METHODS FOR INCREASING  
 INCREASING THE LYSINE  
 AND THREONINE CONTENT  
 NUMBER OF SEQUENCES: 107  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: E. I. DU PONT DE NEMOURS  
 AND COMPANY  
 STREET: 1007 MARKET STREET  
 CITY: WILMINGTON  
 STATE: DELAWARE  
 COUNTRY: U.S.A.  
 ZIP: 19898  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MICROSOFT WORD VERSION 2.00  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/823,771  
 FILING DATE: 24-Mar-1997  
 CLASSIFICATION: <unknown>  
 PRIOR APPLICATION NUMBER: 08/474,633

FILED DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: BARBARA C. SIGGELL  
REGISTRATION NUMBER: 30,684  
REFERENCE/DOCKET NUMBER: BB-1037-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-4931  
TELEFAX: 302-773-0164  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: E. coli  
CELL TYPE: DH5 alpha  
IMMEDIATE SOURCE:  
CLONE: 86-H23  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..88  
OTHER INFORMATION: /function= "synthetic  
storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name= "5.8.8.5"  
SEQUENCE DESCRIPTION: SEQ ID NO: 57:  
US-08-823-771-57  
Query Match  
Best Local Similarity 56.9%; Score 22.4; DB 4; Length 97;  
Best Local Similarity 56.9%; Pred. No. 7.7e+03;  
Matches 41; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 1120 GAGTATGAGGATGACACGAGAGGAGATTAAGGAGTTGGAAGAGTACGAGTGA 1179  
DB 10 GAAGATGAGGCGATGAGAGAGCTGAAGAGATGAGAGAGAGCTGAAGAGATGGA 69  
QY 1180 AGTGAAGAGAA 1191  
DB 70 AGAGAGATGAA 81  
RESULT 33  
PCT-US92-06412-48  
Sequence 48, Application PC/TUS9206412  
GENERAL INFORMATION:  
APPLICANT: Saverio Carl Falco  
APPLICANT: Sharon J. Keeler  
TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containing H  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E.I. du Pont de Nemours and Company  
STREET: 1007 Market Street  
CITY: Wilmington  
STATE: Delaware  
COUNTRY: USA  
ZIP: 19898  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: Macintosh System, 6.0  
SOFTWARE: Microsoft Word, 4.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/06412  
FILING DATE: 19920807  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/743,006

FILED DATE: 9 August 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Linda Axamethy Floyd  
REGISTRATION NUMBER: 33,692  
REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 97 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: E. coli  
CELL TYPE: DH5 alpha  
IMMEDIATE SOURCE:  
CLONE: 86-H23  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..88  
OTHER INFORMATION: /function= "synthetic storage protein"  
/product= "protein"  
/gene= "ssp"  
/standard\_name= "5.8.8.5"  
PCT-US92-06412-48  
Query Match  
Best Local Similarity 56.9%; Score 22.4; DB 5; Length 97;  
Best Local Similarity 56.9%; Pred. No. 7.7e+03;  
Matches 41; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 1120 GAGTATGAGGATGACACGAGAGGAGATTAAGGAGTTGGAAGAGTACGAGTGA 1179  
DB 10 GAAGATGAGGCGATGAGAGAGCTGAAGAGATGAGAGAGAGCTGAAGAGATGGA 69  
QY 1180 AGTGAAGAGAA 1191  
DB 70 AGAGAGATGAA 81  
RESULT 34  
US-08-465-591A-75  
Sequence 75, Application US/08465591A  
Patent No. 5837834  
GENERAL INFORMATION:  
APPLICANT: NIKOS PAGRATIS  
APPLICANT: LARRY GOLD  
TITLE OF INVENTION: HIGH AFFINITY HKGP NUCLEIC  
ACID LIGANDS AND INHIBITORS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson and Bratschun, L.L.C.  
STREET: 8400 East Prentice Avenue, Suite #200  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,591A  
FILING DATE: 5-June 1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 8-SEPTEMBER-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Diane H. McCleard  
REGISTRATION NUMBER: 33,960  
REFERENCE/DOCKET NUMBER: NEX 39-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3433  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-465-594A-75

Query Match 0.4%; Score 22.2; DB 2; Length 71;  
Best Local Similarity 56.9%; Pred. No. 7.3e+03;  
Matches 29; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 31 GAGATCTTTATGACTCTCCGCCAGACACCTCGACAGATGAACGC 81  
DB 17 GACUATCUGGCGUCCAUCCACCCGAGCCGCCGCGCAGACGACUCCG 67

RESULT 35  
US-08-465-594A-75  
Sequence 75 Application US/08465594A  
Patent No. 5846713  
GENERAL INFORMATION:  
APPLICANT: NIKOS PAGRATIS  
APPLICANT: LARRY GOLD  
TITLE OF INVENTION: HIGH AFFINITY HKGE NUCLEIC  
TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS  
NUMBER OF SEQUENCES: 77  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson and Bratschun, L.L.C.  
STREET: 8400 East Prentice Avenue, Suite #200  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,594A  
FILING DATE: 5-JUNE-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/117,991  
FILING DATE: 8-SEPTEMBER-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX 39-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3433  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 75:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-465-594A-75

Query Match 0.4%; Score 22.2; DB 2; Length 71;  
Best Local Similarity 56.9%; Pred. No. 7.3e+03;  
Matches 29; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

OY 31 GAGATCTTTATGACTCTCCGCCAGACACCTCGACAGATGAACGC 81  
DB 17 GACUATCUGGCGUCCAUCCACCCGAGCCGCCGCGCAGACGACUCCG 67

RESULT 36  
US-08-973-124-260  
Sequence 260, Application US/08973124  
Patent No. 6207816  
GENERAL INFORMATION:  
APPLICANT: LARRY GOLD et al.  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
TITLE OF INVENTION: LIGANDS TO GROWTH  
NUMBER OF SEQUENCES: 304  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,124  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08014  
FILING DATE: 30-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,423  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,424  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,594  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,591  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,725  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,783  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/618,693  
FILING DATE: 20-MARCH-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 260:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
FEATURE:  
OTHER INFORMATION: All pyrimidines are 2'-fluor  
US-08-973-124-260

Query Match 0.48; Score 22.2; DB 4; Length 71;  
Best Local Similarity 56.9%; Pred. No. 7.3e+03;  
Matches 29; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 31 GAGATCTTTATGTACTCTCCGCCAGACACCTCGACAGATGAACGC 81  
11 11 : 11 : 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 17 GACUACUGGCGUCCAUCCACCCAGCCGCCGCGCAGACGACUCGC 67

RESULT 37  
PCT-US96-08014-260  
Sequence 260, Application PC/TUS9608014  
GENERAL INFORMATION:  
APPLICANT: LARRY GOLD; NEBOJA JANJIC; STEVEN RINGQUIST;  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH  
TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED  
TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN  
TITLE OF INVENTION: KEROTINOCYTE GROWTH FACTOR (hKGF)  
NUMBER OF SEQUENCES: 304  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08014  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,423  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,424  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,594  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,591  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,725  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,783  
FILING DATE: 07-JUNE-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/618,693  
FILING DATE: 20-MARCH-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 260:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
FEATURE:  
OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'F) modified  
PCT-US96-08014-260

Query Match 0.48; Score 22.2; DB 5; Length 71;  
Best Local Similarity 56.9%; Pred. No. 7.3e+03;  
Matches 29; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

Oy 31 GAGATCTTTATGTACTCTCCGCCAGACACCTCGACAGATGAACGC 81  
11 11 : 11 : 11 11 11 11 11 11 11 11 11 11 11 11 11  
Db 17 GACUACUGGCGUCCAUCCACCCAGCCGCCGCGCAGACGACUCGC 67

RESULT 38  
US-08-488-402A-99/c  
Sequence 99, Application US/08488402A  
GENERAL INFORMATION:  
APPLICANT: GOLD ET AL.  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO  
TITLE OF INVENTION: CHRONIC GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN  
TITLE OF INVENTION: HORMONES  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,402A  
FILING DATE: 07 JUNE 1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/177,991  
FILING DATE: 8-SEPTEMBER-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX36-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 85 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-F modified  
FEATURE:  
OTHER INFORMATION: All U's are 2'-F modified  
US-08-488-402A-99

Query Match 0.4%; Score 22.2; DB 2; Length 85;  
Best Local Similarity 64.7%; Pred. No. 8.1e+03;  
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1280 TTGAGAGCTCGATCTGAGATGATCTCTTGCTGGGAGACACAGACT 1330  
DB 80 TTGTGAGCTCTCTGTCGAGAGATCGTCAATTGACTAGGACCGTTAGCT 30

RESULT 39  
US-08-484-552A-99/c  
Sequence 99, Application US/08484552A  
Patent No. 5849890  
GENERAL INFORMATION:  
APPLICANT: GOLD, LARRY  
APPLICANT: JAYASENA, SUMEDHA  
APPLICANT: NIEUWLANDT, DAN  
APPLICANT: DAVIS, KEN  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE LIGANDS TO CHORIONIC  
TITLE OF INVENTION: GONADOTROPIN HORMONE AND RELATED GLYCOPROTEIN HORMONES  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,552A  
FILING DATE: 07 JUNE 1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/536,428  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/931,473  
FILING DATE: 17-AUGUST-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/177,991  
FILING DATE: 8-SEPTEMBER-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX36-2

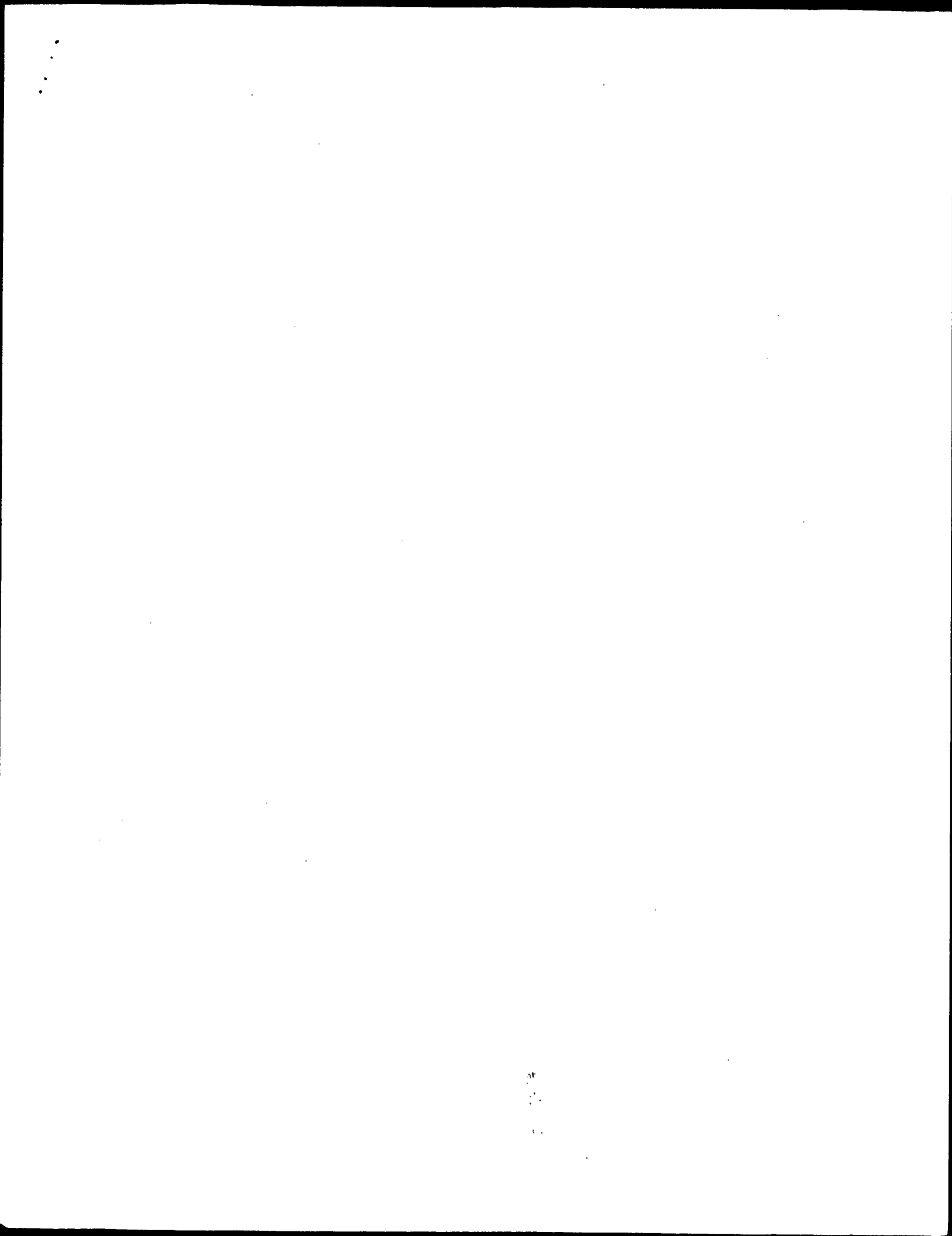
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 85 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-F modified  
FEATURE:  
OTHER INFORMATION: All U's are 2'-F modified  
US-08-484-552A-99

Query Match 0.4%; Score 22.2; DB 2; Length 85;  
Best Local Similarity 64.7%; Pred. No. 8.1e+03;  
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 1280 TTGAGAGCTCGATCTGAGATGATCTCTTGCTGGGAGACACAGACT 1330  
DB 80 TTGTGAGCTCTCTGTCGAGAGATCGTCAATTGACTAGGACCGTTAGCT 30

RESULT 40  
PCT-US96-09472-99/c  
Sequence 99, Application PC/TUS9609472  
GENERAL INFORMATION:  
APPLICANT: GOLD ET AL.  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
TITLE OF INVENTION: LIGANDS TO CHORIONIC GONADOTROPIN HORMONE AND RELATED  
NUMBER OF SEQUENCES: 160  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG  
COMPUTER: IBM pc compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09472  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: 08/488,402  
APPLICATION NUMBER:  
FILING DATE: 07 JUNE 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,552  
FILING DATE: 07 JUNE 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX36-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 85 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
OTHER INFORMATION: All C's are 2'-F modified  
FEATURE:  
OTHER INFORMATION: All U's are 2'-F modified  
PCT-US96-09472-99







GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 09:34:46 ; Search time 122 Seconds  
(without alignments)  
14511.307 Million cell updates/sec

Title: US-09-676-436-3  
Perfect score: 4990  
Sequence: 1 ctgaagactctccgatga.....ggtttatttaggaagctc 4990

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues  
Total number of hits satisfying chosen parameters: 182768

Minimum DB seq length: 8  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :

Published Applications -NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCIT\_NEW\_PUB.seq:\*
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- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26.2	0.5	90	10	US-09-923-876-2711
2	25.8	0.5	81	10	US-09-864-761-31768
3	25	0.5	91	10	US-09-864-761-31768
4	24.8	0.5	92	9	US-09-733-6928-31
5	24.4	0.5	99	10	US-09-864-761-20908
6	24.2	0.5	80	10	US-09-864-761-28769
7	24.2	0.5	95	10	US-09-864-761-28328
8	24.2	0.5	99	10	US-09-864-761-25222
9	23.8	0.5	86	10	US-09-847-113-6
10	23.8	0.5	90	10	US-09-864-761-22288
11	23.8	0.5	100	10	US-09-969-373-453
12	23.6	0.5	79	10	US-09-998-598-1113
13	23.6	0.5	92	10	US-09-783-590-9797
14	23.6	0.5	100	10	US-09-728-445-336
15	23.4	0.5	70	10	US-09-923-876-1834
16	23.2	0.5	89	10	US-09-783-590-9597
17	23.2	0.5	93	10	US-09-864-761-20158
18	23.2	0.5	94	9	US-09-933-797-749
19	23.2	0.5	96	10	US-09-864-761-27858
20	23.2	0.5	96	10	US-09-864-761-32598
21	23.2	0.5	97	10	US-09-864-761-25187
22	23	0.5	84	10	US-09-864-761-25976
23	23	0.5	84	10	US-09-864-761-33084
24	23	0.5	91	10	US-09-864-761-27227
25	23	0.5	95	10	US-09-864-761-27655
26	22.8	0.5	87	10	US-09-864-761-31482
27	22.8	0.5	89	10	US-09-864-761-32824
28	22.8	0.5	98	10	US-09-923-876-1300
29	22.6	0.5	64	10	US-09-919-580-637
30	22.6	0.5	96	10	US-09-878-574-7267
31	22.6	0.5	100	10	US-09-864-761-24215
32	22.6	0.5	83	10	US-09-864-761-25667
33	22.4	0.4	83	10	US-09-878-574-14838
34	22.4	0.4	95	10	US-09-864-761-19403
35	22.4	0.4	100	10	US-09-864-761-27595
36	22.2	0.4	75	10	US-09-864-761-24218
37	22.2	0.4	80	10	US-09-969-373-613
38	22.2	0.4	83	10	US-09-864-761-22604
39	22.2	0.4	86	10	US-09-878-574-5668
40	22.2	0.4	87	10	US-09-191-724-3
41	22.2	0.4	98	10	US-09-878-574-15750
42	22.2	0.4	99	10	US-09-922-261-166
43	22.2	0.4	99	10	US-09-921-798-21
44	22.2	0.4	99	10	US-09-864-761-22288
45	22	0.4	90	10	US-09-923-876-1630
46	22	0.4	91	10	US-09-923-876-1630
47	22	0.4	98	10	US-09-969-373-22
48	21.8	0.4	77	10	US-09-919-580-319
49	21.8	0.4	79	10	US-09-797-223-5
50	21.8	0.4	83	10	US-09-969-373-1387
51	21.8	0.4	85	10	US-09-923-876-19
52	21.8	0.4	90	10	US-09-864-761-20887
53	21.8	0.4	93	10	US-09-971-798-3
54	21.8	0.4	98	10	US-09-864-761-32790
55	21.8	0.4	98	10	US-09-969-373-1345
56	21.6	0.4	99	10	US-09-971-798-20
57	21.6	0.4	100	10	US-09-878-574-7246
58	21.6	0.4	84	9	US-10-046-935-440
59	21.6	0.4	89	10	US-09-864-761-31525
60	21.6	0.4	96	10	US-09-864-761-33294
61	21.6	0.4	96	10	US-09-783-590-4975
62	21.4	0.4	98	10	US-09-864-761-27788
63	21.4	0.4	67	10	US-09-783-590-8768
64	21.4	0.4	76	10	US-09-864-761-21481
65	21.4	0.4	78	10	US-09-864-761-25048
66	21.4	0.4	93	10	US-09-864-761-24680
67	21.4	0.4	93	10	US-09-860-352-13791
68	21.4	0.4	100	10	US-09-864-761-28969
69	21.4	0.4	100	10	US-09-969-373-258
70	21.2	0.4	76	10	US-09-847-113-4
71	21.2	0.4	78	10	US-09-864-761-26577
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73	21.2	0.4	85	10	US-09-864-761-23322
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76	21.2	0.4	93	10	US-09-864-761-32506
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91	21	0.4	92	10	US-09-864-761-21895
92	21	0.4	93	10	US-09-923-876-3591
93	21	0.4	93	10	US-09-864-761-33182
94	21	0.4	94	10	US-09-864-761-261
95	21	0.4	94	10	US-09-864-761-32598
96	21	0.4	94	10	US-09-864-761-25187
97	21	0.4	97	10	US-09-864-761-25976
98	21	0.4	84	10	US-09-864-761-33084
99	21	0.4	84	10	US-09-864-761-27227
100	21	0.4	95	10	US-09-864-761-27655
101	21	0.4	87	10	US-09-864-761-31482
102	21	0.4	89	10	US-09-864-761-32824
103	21	0.4	98	10	US-09-923-876-1300
104	21	0.4	64	10	US-09-919-580-637
105	21	0.4	96	10	US-09-878-574-7267
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108	21	0.4	83	10	US-09-878-574-14838
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110	21	0.4	100	10	US-09-864-761-27595
111	21	0.4	75	10	US-09-864-761-24218
112	21	0.4	80	10	US-09-969-373-613
113	21	0.4	83	10	US-09-864-761-22604
114	21	0.4	86	10	US-09-878-574-5668
115	21	0.4	87	10	US-09-191-724-3
116	21	0.4	98	10	US-09-878-574-15750
117	21	0.4	99	10	US-09-922-261-166
118	21	0.4	99	10	US-09-921-798-21
119	21	0.4	99	10	US-09-864-761-22288
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122	21	0.4	98	10	US-09-969-373-22
123	21	0.4	77	10	US-09-919-580-319
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125	21	0.4	83	10	US-09-969-373-1387
126	21	0.4	85	10	US-09-923-876-19
127	21	0.4	90	10	US-09-864-761-20887
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136	21	0.4	96	10	US-09-783-590-4975
137	21	0.4	98	10	US-09-864-761-27788
138	21	0.4	67	10	US-09-783-590-8768
139	21	0.4	76	10	US-09-864-761-21481
140	21	0.4	78	10	US-09-864-761-25048
141	21	0.4	93	10	US-09-864-761-24680
142	21	0.4	93	10	US-09-860-352-13791
143	21	0.4	100	10	US-09-864-761-28969
144	21	0.4	100	10	US-09-969-373-258
145	21	0.4	76	10	US-09-847-113-4
146	21	0.4	78	10	US-09-864-761-26577
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149	21	0.4	85	10	US-09-864-761-23322
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153	21	0.4	98	10	US-09-864-761-24125
154	21	0.4	99	10	US-09-969-373-384
155	21	0.4	99	10	US-09-864-761-32676
156	21	0.4	99	10	US-09-783-590-12424
157	21	0.4	60	10	US-09-776-695-3
158	21	0.4	77	10	US-09-864-761-17112
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160	21	0.4	78	10	US-09-922-261-323
161	21	0.4	89	10	US-09-864-761-26044
162	21	0.4	89	10	US-09-864-761-32284
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164	21	0.4	91	10	US-09-864-761-22013
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93	21	0.4	95	10	US-09-878-574-920	Sequence 920, App
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105	20.8	0.4	94	10	US-09-864-761-22995	Sequence 22995, A
106	20.8	0.4	95	10	US-09-969-373-656	Sequence 656, App
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113	20.6	0.4	71	10	US-09-756-095-86	Sequence 86, Appl
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116	20.6	0.4	77	8	US-08-978-634-30	Sequence 30, Appl
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118	20.6	0.4	77	8	US-08-978-637-30	Sequence 30, Appl
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123	20.6	0.4	80	10	US-09-923-876-270	Sequence 270, App
124	20.6	0.4	82	10	US-09-923-876-5283	Sequence 5283, App
125	20.6	0.4	82	10	US-09-864-761-26051	Sequence 26051, A
126	20.6	0.4	84	10	US-09-864-761-27108	Sequence 27108, A
127	20.6	0.4	87	10	US-09-864-761-23462	Sequence 23462, A
128	20.6	0.4	88	10	US-09-864-761-31450	Sequence 31450, A
129	20.6	0.4	90	8	US-08-837-459-24	Sequence 24, Appl
130	20.6	0.4	90	10	US-09-864-761-21971	Sequence 21971, A
131	20.6	0.4	92	10	US-09-969-373-314	Sequence 314, App
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134	20.6	0.4	96	9	US-10-046-935-1699	Sequence 1699, Ap
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137	20.6	0.4	98	9	US-09-923-217-992	Sequence 992, App
138	20.6	0.4	98	10	US-09-833-263-392	Sequence 392, App
139	20.6	0.4	98	10	US-09-969-373-115	Sequence 115, App
140	20.6	0.4	98	10	US-09-969-373-115	Sequence 115, App
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143	20.4	0.4	57	9	US-09-783-590-836	Sequence 836, App
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152	20.4	0.4	93	10	US-09-780-669-220	Sequence 220, App
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154	20.4	0.4	93	10	US-09-82-827-220	Sequence 220, App
155	20.4	0.4	93	10	US-09-115-453-220	Sequence 220, App
156	20.4	0.4	95	10	US-09-864-761-32571	Sequence 32571, A
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158	20.4	0.4	96	10	US-09-864-761-30621	Sequence 30621, A
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160	20.4	0.4	97	10	US-09-783-590-6702	Sequence 6702, Ap
161	20.4	0.4	97	10	US-09-969-373-779	Sequence 779, App
162	20.4	0.4	98	10	US-09-960-352-13299	Sequence 13299, A
163	20.4	0.4	99	10	US-09-864-761-17596	Sequence 17596, A
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167	20.2	0.4	57	10	US-09-922-261-428	Sequence 428, App
168	20.2	0.4	67	10	US-09-923-501-759	Sequence 759, App
169	20.2	0.4	66	10	US-09-783-590-8768	Sequence 8768, App
170	20.2	0.4	69	10	US-09-922-217-929	Sequence 929, App
171	20.2	0.4	69	10	US-09-833-263-929	Sequence 929, App
172	20.2	0.4	69	10	US-09-983-965-3899	Sequence 3899, App
173	20.2	0.4	70	10	US-09-263-955-489	Sequence 489, App
174	20.2	0.4	72	10	US-09-923-876-3592	Sequence 3592, App
175	20.2	0.4	75	10	US-09-983-965-223	Sequence 223, App
176	20.2	0.4	78	10	US-09-864-761-26225	Sequence 26225, A
177	20.2	0.4	89	10	US-09-864-761-28181	Sequence 28181, A
178	20.2	0.4	89	10	US-09-864-761-29334	Sequence 29334, A
179	20.2	0.4	90	10	US-09-922-261-376	Sequence 376, App
180	20.2	0.4	91	10	US-09-878-574-5331	Sequence 5331, App
181	20.2	0.4	92	10	US-09-764-877-407	Sequence 407, App
182	20.2	0.4	93	10	US-09-864-761-17259	Sequence 17259, A
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184	20.2	0.4	95	10	US-09-916-940-96	Sequence 96, Appl
185	20.2	0.4	96	10	US-09-764-866-274	Sequence 274, App
186	20.2	0.4	97	10	US-09-923-876-4405	Sequence 4405, App
187	20.2	0.4	97	10	US-09-960-352-13934	Sequence 13934, A
188	20.2	0.4	98	10	US-09-963-373-427	Sequence 427, App
189	20.2	0.4	98	10	US-09-960-352-2100	Sequence 2100, App
190	20.2	0.4	99	10	US-09-864-761-29067	Sequence 29067, A
191	20.2	0.4	99	10	US-09-864-761-12354	Sequence 12354, A
192	20.2	0.4	99	10	US-09-960-352-699	Sequence 699, App
193	20.2	0.4	100	10	US-09-770-686-907	Sequence 907, App
194	20.2	0.4	100	10	US-09-924-035A-426	Sequence 426, App
195	20	0.4	51	10	US-09-976-787-25	Sequence 25, Appl
196	20	0.4	51	10	US-09-967-013-81	Sequence 81, Appl
197	20	0.4	56	10	US-09-967-013-81	Sequence 81, Appl
198	20	0.4	56	10	US-09-967-013-82	Sequence 82, Appl
199	20	0.4	59	10	US-09-967-013-82	Sequence 82, Appl
200	20	0.4	59	10	US-09-967-013-88	Sequence 88, Appl
201	20	0.4	59	10	US-09-967-013-89	Sequence 89, Appl
202	20	0.4	65	10	US-09-878-574-10483	Sequence 10483, A
203	20	0.4	67	12	US-09-920-300A-799	Sequence 799, App
204	20	0.4	67	12	US-10-033-528-799	Sequence 799, App
205	20	0.4	69	10	US-09-785-632-38	Sequence 38, Appl
206	20	0.4	70	10	US-09-983-965-417	Sequence 417, App
207	20	0.4	73	10	US-09-923-876-3060	Sequence 3060, Ap
208	20	0.4	77	10	US-09-864-761-29497	Sequence 29497, A
209	20	0.4	78	10	US-09-878-574-3746	Sequence 3746, Ap
210	20	0.4	80	10	US-09-764-877-445	Sequence 445, App
211	20	0.4	80	10	US-09-788-297-7	Sequence 7, Appli
212	20	0.4	80	10	US-09-969-373-613	Sequence 613, App
213	20	0.4	83	10	US-09-284-0939-894	Sequence 894, App
214	20	0.4	87	10	US-09-864-761-17846	Sequence 17846, A
215	20	0.4	88	10	US-09-864-761-19737	Sequence 19737, A
216	20	0.4	88	10	US-09-864-761-31192	Sequence 31192, A
217	20	0.4	89	10	US-09-864-761-31259	Sequence 31259, A
218	20	0.4	89	10	US-09-864-761-31259	Sequence 31259, A
219	20	0.4	89	10	US-09-983-965-1255	Sequence 1255, Ap
220	20	0.4	89	10	US-09-883-965-1255	Sequence 1255, Ap
221	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
222	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
223	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
224	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
225	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
226	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
227	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
228	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
229	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
230	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
231	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
232	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
233	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
234	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
235	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
236	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
237	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap
238	20	0.4	90	10	US-09-815-242-3495	Sequence 3495, Ap

239	19.8	0.4	63	10	US-09-811-672-4	Sequence 4, Appl 1	312	19.6	0.4	96	10	US-09-864-761-33016	Sequence 33016, A
240	19.8	0.4	63	10	US-09-983-965-2679	Sequence 2679, Ap	313	19.6	0.4	96	10	US-09-783-590-2031	Sequence 2031, A
241	19.8	0.4	66	10	US-09-886-886A-13	Sequence 13, Appl	314	19.6	0.4	96	10	US-09-912-679-32	Sequence 32, Appl
242	19.8	0.4	75	10	US-09-758-140-9	Sequence 9, Appl 1	315	19.6	0.4	98	10	US-09-864-761-19650	Sequence 19650, A
243	19.8	0.4	75	10	US-09-972-599A-93	Sequence 9, Appl 1	316	19.6	0.4	98	10	US-09-864-761-30912	Sequence 30912, A
244	19.8	0.4	75	10	US-09-972-599A-93	Sequence 9, Appl 1	317	19.6	0.4	100	10	US-09-969-573-1195	Sequence 1195, A
245	19.8	0.4	75	10	US-09-820-339A-3	Sequence 3, Appl 1	318	19.6	0.4	45	10	US-09-827-289-11	Sequence 11, Appl 1
246	19.8	0.4	76	10	US-09-864-761-26408	Sequence 26408, A	319	19.4	0.4	61	10	US-09-795-668-1342	Sequence 1342, Ap
247	19.8	0.4	76	10	US-09-864-761-31800	Sequence 31800, A	320	19.4	0.4	61	10	US-09-795-668-1342	Sequence 1342, Ap
248	19.8	0.4	77	10	US-09-864-761-22941	Sequence 22941, A	321	19.4	0.4	62	10	US-09-912-679-31	Sequence 31, Appl 1
249	19.8	0.4	77	10	US-09-878-574-10313	Sequence 10313, A	322	19.4	0.4	62	10	US-09-795-668-1303	Sequence 1303, Ap
250	19.8	0.4	79	10	US-09-919-580-499	Sequence 499, App	323	19.4	0.4	63	10	US-09-983-965-5121	Sequence 5121, Ap
251	19.8	0.4	80	10	US-09-827-289-7	Sequence 7, Appl 1	324	19.4	0.4	68	10	US-09-923-246-79	Sequence 79, Appl 1
252	19.8	0.4	80	10	US-09-827-289-8	Sequence 8, Appl 1	325	19.4	0.4	71	10	US-09-823-250-31	Sequence 31, Appl 1
253	19.8	0.4	81	10	US-09-864-761-26536	Sequence 26536, A	326	19.4	0.4	73	10	US-09-263-959-724	Sequence 724, App
254	19.8	0.4	82	10	US-09-864-761-33039	Sequence 33039, A	327	19.4	0.4	75	10	US-09-864-761-27031	Sequence 27031, A
255	19.8	0.4	84	10	US-09-864-761-18641	Sequence 18641, A	328	19.4	0.4	78	10	US-09-922-661-378	Sequence 378, App
256	19.8	0.4	87	10	US-09-864-761-25749	Sequence 25749, A	329	19.4	0.4	80	10	US-09-864-761-25594	Sequence 25594, A
257	19.8	0.4	87	10	US-09-864-761-31365	Sequence 31365, A	330	19.4	0.4	80	10	US-09-864-761-28951	Sequence 28951, A
258	19.8	0.4	87	10	US-09-864-761-24761	Sequence 24761, A	331	19.4	0.4	81	10	US-09-864-761-22617	Sequence 22617, A
259	19.8	0.4	88	10	US-09-864-761-4255	Sequence 4255, Ap	332	19.4	0.4	82	10	US-09-969-373-1056	Sequence 1056, Ap
260	19.8	0.4	89	10	US-09-883-965-4255	Sequence 4255, Ap	333	19.4	0.4	82	10	US-09-772-719-17	Sequence 37, Appl 1
261	19.8	0.4	90	10	US-09-864-761-26294	Sequence 26294, A	334	19.4	0.4	84	10	US-09-878-574-1869	Sequence 1869, Ap
262	19.8	0.4	90	10	US-09-864-761-27224	Sequence 27224, A	335	19.4	0.4	85	10	US-09-864-761-18967	Sequence 18967, A
263	19.8	0.4	90	10	US-09-972-599A-31	Sequence 31, Appl 1	336	19.4	0.4	87	10	US-09-864-761-22909	Sequence 22909, A
264	19.8	0.4	91	10	US-09-864-761-31491	Sequence 31491, A	337	19.4	0.4	87	10	US-09-864-761-27857	Sequence 27857, A
265	19.8	0.4	91	10	US-09-960-352-306	Sequence 306, Ap	338	19.4	0.4	87	10	US-10-024-997-88	Sequence 88, Appl 1
266	19.8	0.4	94	10	US-09-215-652-7	Sequence 7, Appl 1	339	19.4	0.4	87	12	US-09-864-761-29875	Sequence 2715, Ap
267	19.8	0.4	94	10	US-09-878-574-7191	Sequence 7191, Ap	340	19.4	0.4	88	10	US-09-983-965-2716	Sequence 2, Appl 1
268	19.8	0.4	95	10	US-09-960-352-3523	Sequence 3523, Ap	341	19.4	0.4	90	10	US-09-917-330-2	Sequence 17072, A
269	19.8	0.4	96	10	US-09-878-574-5248	Sequence 5248, Ap	342	19.4	0.4	90	10	US-09-864-761-17072	Sequence 17072, A
270	19.8	0.4	96	10	US-09-878-574-5248	Sequence 5248, Ap	343	19.4	0.4	92	10	US-09-864-761-18968	Sequence 18968, A
271	19.8	0.4	96	10	US-09-878-574-5248	Sequence 5248, Ap	344	19.4	0.4	92	10	US-09-864-761-18968	Sequence 18968, A
272	19.8	0.4	96	10	US-09-969-373-551	Sequence 551, App	345	19.4	0.4	93	10	US-09-969-373-719	Sequence 719, App
273	19.8	0.4	98	10	US-09-777-564-865	Sequence 865, App	346	19.4	0.4	95	10	US-09-864-761-32571	Sequence 32571, A
274	19.8	0.4	98	10	US-09-864-761-24557	Sequence 24557, A	347	19.4	0.4	95	10	US-09-960-352-6975	Sequence 6975, Ap
275	19.8	0.4	98	10	US-09-783-590-9853	Sequence 9853, Ap	348	19.4	0.4	96	10	US-09-864-761-151364	Sequence 151, App
276	19.8	0.4	99	10	US-09-864-761-38045	Sequence 38045, A	349	19.4	0.4	98	10	US-09-969-373-431	Sequence 431, App
277	19.8	0.4	99	10	US-09-864-761-38045	Sequence 38045, A	350	19.4	0.4	99	10	US-09-864-761-24821	Sequence 24821, A
278	19.8	0.4	99	10	US-09-815-242-1049	Sequence 1049, Ap	351	19.4	0.4	99	10	US-09-969-373-431	Sequence 431, App
279	19.8	0.4	100	10	US-09-783-590-10893	Sequence 10893, A	352	19.4	0.4	99	10	US-09-969-373-431	Sequence 431, App
280	19.8	0.4	100	10	US-09-867-701-2268	Sequence 2268, Ap	353	19.2	0.4	69	10	US-09-783-590-8150	Sequence 8150, Ap
281	19.6	0.4	9	9	US-09-992-598-45	Sequence 45, Appl	354	19.2	0.4	72	10	US-09-927-850-27	Sequence 27, Appl 1
282	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	355	19.2	0.4	72	10	US-09-864-761-26979	Sequence 26979, A
283	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	356	19.2	0.4	75	10	US-09-864-761-26979	Sequence 26979, A
284	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	357	19.2	0.4	77	10	US-09-922-217-324	Sequence 2406, A
285	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	358	19.2	0.4	78	10	US-09-922-217-324	Sequence 324, App
286	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	359	19.2	0.4	78	10	US-09-922-217-324	Sequence 28847, A
287	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	360	19.2	0.4	79	10	US-09-864-761-25883	Sequence 1236, Ap
288	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	361	19.2	0.4	83	10	US-09-864-761-25883	Sequence 28847, A
289	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	362	19.2	0.4	83	10	US-09-864-761-25883	Sequence 28847, A
290	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	363	19.2	0.4	84	10	US-09-864-761-25883	Sequence 28847, A
291	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	364	19.2	0.4	85	10	US-09-864-761-25883	Sequence 28847, A
292	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	365	19.2	0.4	85	10	US-09-864-761-25883	Sequence 28847, A
293	19.6	0.4	50	10	US-09-989-722-45	Sequence 45, Appl	366	19.2	0.4	85	10	US-09-864-761-25883	Sequence 28847, A
294	19.6	0.4	56	10	US-09-738-363-25	Sequence 25, Appl	367	19.2	0.4	86	12	US-09-965-099-82	Sequence 82, Appl 1
295	19.6	0.4	67	10	US-09-815-242-1629	Sequence 1629, Ap	368	19.2	0.4	86	12	US-09-965-099-82	Sequence 82, Appl 1
296	19.6	0.4	68	10	US-09-909-652-6	Sequence 6, Appl 1	369	19.2	0.4	87	10	US-09-864-761-31392	Sequence 31392, A
297	19.6	0.4	81	10	US-09-864-761-12637	Sequence 12637, A	370	19.2	0.4	87	10	US-09-864-761-31392	Sequence 31392, A
298	19.6	0.4	81	10	US-09-864-761-12637	Sequence 12637, A	371	19.2	0.4	88	10	US-09-864-761-31392	Sequence 31392, A
299	19.6	0.4	82	10	US-09-864-761-20574	Sequence 20574, A	372	19.2	0.4	88	10	US-09-864-761-31392	Sequence 31392, A
300	19.6	0.4	85	10	US-09-864-761-22337	Sequence 22337, A	373	19.2	0.4	88	10	US-09-864-761-31392	Sequence 31392, A
301	19.6	0.4	85	10	US-09-864-761-22337	Sequence 22337, A	374	19.2	0.4	88	10	US-09-864-761-31392	Sequence 31392, A
302	19.6	0.4	86	10	US-09-878-574-9984	Sequence 9984, Ap	375	19.2	0.4	91	10	US-09-971-798-6	Sequence 6, Appl 1
303	19.6	0.4	87	9	US-09-933-797-135	Sequence 135, App	376	19.2	0.4	91	12	US-09-965-099-18	Sequence 18, Appl 1
304	19.6	0.4	88	10	US-09-864-761-18623	Sequence 18623, A	377	19.2	0.4	92	10	US-10-051-852-18	Sequence 3, Appl 1
305	19.6	0.4	88	10	US-09-864-761-21403	Sequence 21403, A	378	19.2	0.4	92	10	US-09-878-574-1894	Sequence 1894, Ap
306	19.6	0.4	89	10	US-09-969-373-346	Sequence 346, App	379	19.2	0.4	93	10	US-09-878-574-1894	Sequence 1894, Ap
307	19.6	0.4	89	10	US-09-864-761-27643	Sequence 27643, A	380	19.2	0.4	93	10	US-09-864-761-27643	Sequence 27643, A
308	19.6	0.4	93	10	US-09-864-761-24209	Sequence 24209, A	381	19.2	0.4	93	10	US-09-864-761-24209	Sequence 24209, A
309	19.6	0.4	94	10	US-09-864-761-29215	Sequence 29215, A	382	19.2	0.4	96	10	US-09-864-761-29215	Sequence 29215, A
310	19.6	0.4	96	9	US-10-046-935-1699	Sequence 1699, Ap	383	19.2	0.4	96	10	US-09-864-761-29215	Sequence 29215, A
311	19.6	0.4	96	10	US-09-864-761-30492	Sequence 30492, A	384	19.2	0.4	96	10	US-09-864-761-30492	Sequence 30492, A

C 385	19.2	0.4	97	10	US-09-969-373-950	Sequence 950, App	458	19	0.4	96	10	US-09-864-761-25639	Sequence 25639, A
C 387	19.2	0.4	98	10	US-09-864-761-26598	Sequence 26598, A	459	19	0.4	97	10	US-09-294-093B-840	Sequence 840, App
C 388	19.2	0.4	99	10	US-09-864-761-30787	Sequence 30787, A	C 460	19	0.4	97	10	US-09-864-761-27662	Sequence 27662, A
C 389	19.2	0.4	100	10	US-09-867-701-5615	Sequence 5615, Ap	C 461	19	0.4	98	10	US-09-783-590-9853	Sequence 9853, Ap
C 390	19.2	0.4	100	10	US-09-864-761-28542	Sequence 28542, A	C 462	19	0.4	99	10	US-09-864-761-32475	Sequence 32475, A
C 391	19.2	0.4	100	10	US-09-783-590-6064	Sequence 6064, Ap	C 463	19	0.4	99	12	US-10-033-558-1823	Sequence 1823, Ap
C 392	19.2	0.4	100	10	US-09-999-672-15	Sequence 15, Appl	C 464	19	0.4	100	10	US-09-864-761-18879	Sequence 18879, A
C 393	19.2	0.4	100	10	US-09-969-373-30	Sequence 30, Appl	C 465	19	0.4	100	10	US-09-864-761-24828	Sequence 24828, A
C 394	19.2	0.4	100	10	US-09-983-965-296	Sequence 296, App	C 466	19	0.4	100	10	US-09-864-761-251003	Sequence 251003, A
C 395	19.2	0.4	100	12	US-09-924-035A-289	Sequence 289, App	C 467	19	0.4	100	10	US-09-828-303-41	Sequence 6085, Ap
C 396	19.2	0.4	47	10	US-09-765-527-244	Sequence 15, Appl	C 468	18.8	0.4	32	10	US-09-864-761-1003	Sequence 41, Appl
C 397	19	0.4	49	10	US-09-179-536B-197	Sequence 244, App	C 469	18.8	0.4	37	10	US-09-882-303-58	Sequence 58, Appl
C 398	19	0.4	50	10	US-09-179-536B-198	Sequence 197, App	C 470	18.8	0.4	32	10	US-09-882-303-58	Sequence 7, Appl1
C 399	19	0.4	51	10	US-09-179-536B-199	Sequence 198, App	C 471	18.8	0.4	45	12	US-10-029-907-13	Sequence 13, Appl1
C 400	19	0.4	52	10	US-09-179-536B-200	Sequence 199, App	C 472	18.8	0.4	47	10	US-09-756-095-71	Sequence 71, Appl
C 401	19	0.4	53	10	US-09-179-536B-201	Sequence 200, App	C 473	18.8	0.4	54	10	US-09-147-142-23	Sequence 23, Appl
C 402	19	0.4	54	10	US-09-179-536B-202	Sequence 201, App	C 474	18.8	0.4	54	10	US-09-147-142-26	Sequence 26, Appl
C 403	19	0.4	55	10	US-09-922-261-325	Sequence 202, App	C 475	18.8	0.4	60	10	US-09-294-093B-5594	Sequence 5594, Ap
C 404	19	0.4	55	10	US-09-179-536B-203	Sequence 203, App	C 476	18.8	0.4	64	10	US-09-864-761-15	Sequence 14, Appl
C 405	19	0.4	56	10	US-09-179-536B-204	Sequence 204, App	C 477	18.8	0.4	65	12	US-10-021-758-41	Sequence 15, Appl
C 406	19	0.4	57	10	US-09-848-164-49	Sequence 49, Appl	C 478	18.8	0.4	66	10	US-09-783-590-9281	Sequence 9281, Ap
C 407	19	0.4	57	10	US-09-179-536B-205	Sequence 205, App	C 479	18.8	0.4	67	10	US-09-887-384A-10	Sequence 10, Appl
C 408	19	0.4	58	10	US-09-179-536B-206	Sequence 206, App	C 480	18.8	0.4	67	10	US-09-815-242-1629	Sequence 1629, Ap
C 409	19	0.4	59	10	US-09-179-536B-207	Sequence 207, App	C 481	18.8	0.4	69	10	US-09-851-190A-12	Sequence 12, Appl
C 410	19	0.4	60	10	US-09-179-536B-208	Sequence 208, App	C 482	18.8	0.4	69	10	US-09-851-190A-12	Sequence 12, Appl
C 411	19	0.4	61	10	US-09-179-536B-209	Sequence 209, App	C 483	18.8	0.4	71	10	US-09-878-574-13067	Sequence 13067, A
C 412	19	0.4	62	10	US-09-179-536B-210	Sequence 210, App	C 484	18.8	0.4	72	9	US-09-832-659-22	Sequence 22, Appl
C 413	19	0.4	62	10	US-09-955-037-1	Sequence 1, Appl1	C 485	18.8	0.4	72	10	US-09-812-679-29	Sequence 29, Appl
C 414	19	0.4	63	10	US-09-179-536B-211	Sequence 211, App	C 486	18.8	0.4	74	10	US-09-294-093B-3534	Sequence 3534, Ap
C 415	19	0.4	64	10	US-09-179-536B-212	Sequence 212, App	C 487	18.8	0.4	75	10	US-09-983-965-223	Sequence 223, App
C 416	19	0.4	65	10	US-09-179-536B-213	Sequence 213, App	C 488	18.8	0.4	76	10	US-09-960-352-6176	Sequence 6176, Ap
C 417	19	0.4	66	10	US-09-179-536B-214	Sequence 214, App	C 489	18.8	0.4	77	10	US-09-923-876-1833	Sequence 1833, Ap
C 418	19	0.4	67	10	US-09-179-536B-215	Sequence 215, App	C 490	18.8	0.4	77	10	US-09-864-761-33023	Sequence 33023, Ap
C 419	19	0.4	68	10	US-09-179-536B-216	Sequence 216, App	C 491	18.8	0.4	80	10	US-09-157-748-43	Sequence 43, Appl
C 420	19	0.4	69	10	US-09-179-536B-217	Sequence 217, App	C 492	18.8	0.4	80	10	US-09-864-761-20481	Sequence 20481, A
C 421	19	0.4	70	10	US-09-179-536B-218	Sequence 218, App	C 493	18.8	0.4	80	10	US-09-864-761-23803	Sequence 23803, A
C 422	19	0.4	71	10	US-09-179-536B-219	Sequence 219, App	C 494	18.8	0.4	80	10	US-09-864-761-27154	Sequence 27154, A
C 423	19	0.4	72	10	US-09-179-536B-220	Sequence 220, App	C 495	18.8	0.4	80	10	US-09-764-846-267	Sequence 267, App
C 424	19	0.4	73	10	US-09-888-260-56	Sequence 220, App	C 496	18.8	0.4	80	10	US-09-764-846-267	Sequence 267, App
C 425	19	0.4	73	10	US-09-823-876-60	Sequence 56, Appl	C 497	18.8	0.4	80	10	US-09-764-846-267	Sequence 267, App
C 426	19	0.4	73	10	US-09-869-373-87	Sequence 87, Appl	C 498	18.8	0.4	81	9	US-10-046-335-1614	Sequence 1614, Ap
C 427	19	0.4	73	10	US-09-983-965-5268	Sequence 5268, Ap	C 499	18.8	0.4	81	10	US-09-925-301-764	Sequence 764, App
C 428	19	0.4	75	10	US-09-758-140-7	Sequence 7, Appl1	C 500	18.8	0.4	82	10	US-09-864-761-33505	Sequence 33505, A
C 429	19	0.4	75	10	US-09-864-761-25911	Sequence 25911, A	C 501	18.8	0.4	82	10	US-09-878-574-3398	Sequence 3398, Ap
C 430	19	0.4	76	10	US-09-972-599A-7	Sequence 7, Appl1	C 502	18.8	0.4	83	10	US-09-294-093B-3319	Sequence 3319, Ap
C 431	19	0.4	76	10	US-09-864-761-28047	Sequence 28047, A	C 503	18.8	0.4	85	10	US-09-781-804-55	Sequence 2219, Ap
C 432	19	0.4	76	10	US-09-864-761-31463	Sequence 31463, A	C 504	18.8	0.4	85	10	US-09-864-761-28595	Sequence 55, Appl
C 433	19	0.4	76	10	US-09-878-574-5227	Sequence 5227, Ap	C 505	18.8	0.4	86	10	US-09-960-352-11632	Sequence 11632, A
C 434	19	0.4	77	10	US-09-783-590-3207	Sequence 3207, Ap	C 506	18.8	0.4	86	10	US-09-864-761-22876	Sequence 22876, A
C 435	19	0.4	78	10	US-09-179-536B-25	Sequence 25, Appl	C 507	18.8	0.4	87	10	US-09-864-761-33058	Sequence 33058, A
C 436	19	0.4	78	10	US-09-864-761-23374	Sequence 23374, A	C 508	18.8	0.4	87	10	US-09-893-737-135	Sequence 135, App
C 437	19	0.4	79	9	US-09-733-692A-4	Sequence 4, Appl1	C 509	18.8	0.4	87	10	US-09-764-877-2984	Sequence 2984, Ap
C 438	19	0.4	79	10	US-09-864-761-20590	Sequence 20590, A	C 510	18.8	0.4	87	10	US-09-764-877-2984	Sequence 2984, Ap
C 439	19	0.4	80	10	US-09-864-761-31577	Sequence 31577, A	C 511	18.8	0.4	87	10	US-09-764-877-2984	Sequence 2984, Ap
C 440	19	0.4	81	9	US-10-046-935-520	Sequence 520, App	C 512	18.8	0.4	88	10	US-09-815-343-379	Sequence 379, App
C 441	19	0.4	81	10	US-09-864-761-21838	Sequence 21838, A	C 513	18.8	0.4	88	10	US-09-764-869-1992	Sequence 1992, App
C 442	19	0.4	81	10	US-09-909-207-7	Sequence 7, Appl1	C 514	18.8	0.4	88	10	US-09-334-923A-13	Sequence 13, Appl
C 443	19	0.4	81	10	US-09-949-559-115	Sequence 115, App	C 515	18.8	0.4	88	10	US-09-334-923A-13	Sequence 13, Appl
C 444	19	0.4	81	10	US-09-864-761-23322	Sequence 23322, A	C 516	18.8	0.4	88	10	US-09-334-923A-13	Sequence 13, Appl
C 445	19	0.4	85	10	US-09-864-761-25948	Sequence 25948, A	C 517	18.8	0.4	88	10	US-09-334-923A-13	Sequence 13, Appl
C 446	19	0.4	85	10	US-09-864-761-25948	Sequence 25948, A	C 518	18.8	0.4	88	10	US-09-334-923A-13	Sequence 13, Appl
C 447	19	0.4	87	10	US-09-864-761-21228	Sequence 21228, A	C 519	18.8	0.4	89	10	US-09-864-761-20966	Sequence 20966, A
C 448	19	0.4	88	10	US-09-864-761-30180	Sequence 30180, A	C 520	18.8	0.4	89	10	US-09-864-761-23401	Sequence 23401, A
C 449	19	0.4	89	10	US-09-864-761-32525	Sequence 32525, A	C 521	18.8	0.4	89	10	US-09-864-761-23401	Sequence 23401, A
C 450	19	0.4	90	12	US-10-003-496-7	Sequence 7, Appl1	C 522	18.8	0.4	89	10	US-09-925-301-774	Sequence 29473, A
C 451	19	0.4	91	10	US-09-864-761-24801	Sequence 24801, A	C 523	18.8	0.4	90	10	US-09-864-761-23699	Sequence 23699, A
C 452	19	0.4	91	10	US-09-864-761-30056	Sequence 30056, A	C 524	18.8	0.4	91	10	US-09-294-093B-1011	Sequence 1011, Ap
C 453	19	0.4	92	10	US-09-923-876-4530	Sequence 4530, Ap	C 525	18.8	0.4	91	10	US-09-864-761-21126	Sequence 21126, A
C 454	19	0.4	92	10	US-09-923-876-6277	Sequence 6277, Ap	C 526	18.8	0.4	91	10	US-09-864-761-24801	Sequence 24801, A
C 455	19	0.4	93	10	US-09-864-761-30602	Sequence 30602, A	C 527	18.8	0.4	91	10	US-09-864-761-25295	Sequence 25295, A
C 456	19	0.4	93	10	US-09-969-373-42	Sequence 42, Appl	C 528	18.8	0.4	91	10	US-09-815-242-707	Sequence 707, App
C 457	19	0.4	95	10	US-09-864-761-21583	Sequence 21583, A	C 529	18.8	0.4	91	10	US-09-878-574-5331	Sequence 5331, Ap
							C 530	18.8	0.4	92	9	US-09-933-797-542	Sequence 542, App

531	18.8	0.4	92	10	US-09-864-761-25024	Sequence 25024, A	604	18.6	0.4	81	10	US-09-864-761-18720	Sequence 18720, A
532	18.8	0.4	92	12	US-10-029-913-3	Sequence 3, Appl1	605	18.6	0.4	81	10	US-09-864-761-26281	Sequence 26281, A
533	18.8	0.4	93	10	US-09-878-574-15698	Sequence 15698, A	606	18.6	0.4	81	10	US-09-815-242-566	Sequence 566, App
534	18.8	0.4	93	10	US-09-960-352-4510	Sequence 4510, Ap	607	18.6	0.4	81	10	US-09-922-651-251	Sequence 251, App
535	18.8	0.4	93	10	US-09-960-352-13791	Sequence 13791, A	608	18.6	0.4	82	10	US-09-777-564-1655	Sequence 1655, Ap
536	18.8	0.4	94	10	US-09-864-761-33109	Sequence 33109, A	609	18.6	0.4	82	10	US-09-864-761-20295	Sequence 20295, A
537	18.8	0.4	95	9	US-09-933-797-626	Sequence 626, App	610	18.6	0.4	84	9	US-10-060-841-8	Sequence 8, Appl1
538	18.8	0.4	95	10	US-09-864-761-31953	Sequence 31953, A	611	18.6	0.4	84	10	US-09-864-761-24579	Sequence 24579, A
539	18.8	0.4	95	10	US-09-878-574-993	Sequence 993, App	612	18.6	0.4	84	10	US-09-864-761-28712	Sequence 28712, A
540	18.8	0.4	95	10	US-09-919-580-246	Sequence 246, App	613	18.6	0.4	85	10	US-09-864-761-29373	Sequence 29373, A
541	18.8	0.4	95	10	US-09-969-373-1530	Sequence 1530, Ap	614	18.6	0.4	85	10	US-09-960-352-6425	Sequence 6425, Ap
542	18.8	0.4	95	10	US-09-864-761-20356	Sequence 20356, A	615	18.6	0.4	86	10	US-09-864-761-1628	Sequence 1628, Ap
543	18.8	0.4	96	10	US-09-864-761-26318	Sequence 26318, A	616	18.6	0.4	87	10	US-09-864-761-30207	Sequence 30207, A
544	18.8	0.4	96	10	US-09-864-761-33003	Sequence 33003, A	617	18.6	0.4	87	10	US-09-864-761-1904	Sequence 1904, Ap
545	18.8	0.4	96	10	US-09-963-963-2407	Sequence 2407, A	618	18.6	0.4	87	10	US-09-783-590-6677	Sequence 6677, Ap
546	18.8	0.4	96	10	US-09-938-938-5580	Sequence 5580, Ap	619	18.6	0.4	88	12	US-10-024-997-96	Sequence 96, Appl
547	18.8	0.4	97	10	US-09-923-876-2708	Sequence 2708, Ap	620	18.6	0.4	88	10	US-09-864-761-19599	Sequence 19599, A
548	18.8	0.4	97	10	US-09-864-761-22933	Sequence 22933, A	621	18.6	0.4	89	10	US-09-864-761-23367	Sequence 23367, A
549	18.8	0.4	97	10	US-09-815-242-306	Sequence 306, App	622	18.6	0.4	90	10	US-09-927-599A-25	Sequence 25, Appl
550	18.8	0.4	97	10	US-09-969-373-532	Sequence 532, App	623	18.6	0.4	90	10	US-09-878-574-5130	Sequence 5130, Ap
551	18.8	0.4	98	10	US-09-864-761-21839	Sequence 21839, A	624	18.6	0.4	90	10	US-09-864-761-17805	Sequence 17805, A
552	18.8	0.4	98	10	US-09-864-761-24634	Sequence 24634, A	625	18.6	0.4	91	10	US-09-864-761-18674	Sequence 18674, A
553	18.8	0.4	98	10	US-09-878-574-3830	Sequence 3830, Ap	626	18.6	0.4	91	10	US-09-864-761-32561	Sequence 32561, A
554	18.8	0.4	98	10	US-09-878-574-15211	Sequence 15211, A	627	18.6	0.4	91	10	US-09-815-242-1782	Sequence 1782, Ap
555	18.8	0.4	98	10	US-09-864-761-17733	Sequence 2244, Ap	628	18.6	0.4	91	10	US-09-815-242-1786	Sequence 1786, Ap
556	18.8	0.4	99	10	US-09-815-242-2244	Sequence 2244, Ap	629	18.6	0.4	91	10	US-09-783-590-11400	Sequence 11400, A
557	18.8	0.4	99	10	US-09-815-242-2101	Sequence 2101, Ap	630	18.6	0.4	91	10	US-09-923-876-5032	Sequence 5032, Ap
558	18.8	0.4	99	12	US-10-098-035-5	Sequence 5, Appl1	631	18.6	0.4	92	10	US-09-923-876-31063	Sequence 31063, A
559	18.8	0.4	99	12	US-09-770-696-306	Sequence 906, App	632	18.6	0.4	92	10	US-09-838-386-24	Sequence 24, Appl
560	18.8	0.4	100	10	US-09-864-761-28443	Sequence 28443, A	633	18.6	0.4	93	10	US-09-864-761-28408	Sequence 28408, A
561	18.8	0.4	100	10	US-09-728-446-106	Sequence 106, App	634	18.6	0.4	94	10	US-09-755-830-10	Sequence 10, Appl
562	18.8	0.4	100	10	US-09-919-580-428	Sequence 428, App	635	18.6	0.4	94	10	US-09-864-761-22634	Sequence 22634, A
563	18.8	0.4	100	10	US-09-919-580-428	Sequence 57, Appl	636	18.6	0.4	95	10	US-09-864-761-22634	Sequence 22634, A
564	18.8	0.4	100	10	US-09-908-855-57	Sequence 9381, Ap	637	18.6	0.4	95	10	US-09-864-761-31173	Sequence 31173, A
565	18.8	0.4	100	10	US-09-867-701-9381	Sequence 390, App	638	18.6	0.4	95	10	US-09-864-761-31173	Sequence 31173, A
566	18.8	0.4	41	10	US-09-765-272-390	Sequence 302, App	639	18.6	0.4	96	10	US-09-864-761-31173	Sequence 31173, A
567	18.8	0.4	50	10	US-09-179-536B-302	Sequence 302, App	640	18.6	0.4	96	10	US-09-864-761-31173	Sequence 31173, A
568	18.8	0.4	53	10	US-09-746-359A-103	Sequence 303, App	641	18.6	0.4	97	10	US-09-923-876-2708	Sequence 2708, Ap
569	18.8	0.4	53	10	US-09-841-132-37	Sequence 37, Appl	642	18.6	0.4	97	10	US-09-864-761-23281	Sequence 23281, A
570	18.8	0.4	53	10	US-09-874-547-52	Sequence 52, Appl	643	18.6	0.4	97	10	US-09-864-761-23281	Sequence 23281, A
571	18.8	0.4	53	10	US-09-866-514-6	Sequence 5, Appl1	644	18.6	0.4	97	10	US-09-864-761-23281	Sequence 23281, A
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573	18.8	0.4	57	10	US-09-823-634A-5	Sequence 5, Appl1	646	18.6	0.4	99	10	US-09-864-761-23281	Sequence 23281, A
574	18.8	0.4	57	10	US-09-823-634A-5	Sequence 5, Appl1	647	18.6	0.4	99	10	US-09-864-761-23281	Sequence 23281, A
575	18.8	0.4	57	10	US-09-823-634A-5	Sequence 5, Appl1	648	18.6	0.4	99	10	US-09-864-761-23281	Sequence 23281, A
576	18.8	0.4	61	10	US-09-793-666-1328	Sequence 1328, Ap	649	18.6	0.4	99	10	US-09-864-761-23281	Sequence 23281, A
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580	18.8	0.4	63	10	US-09-525-142-1	Sequence 13, Appl1	653	18.6	0.4	100	10	US-09-864-761-18246	Sequence 18246, Ap
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585	18.8	0.4	66	10	US-09-821-831-5	Sequence 1, Appl1	658	18.6	0.4	100	12	US-10-103-855-32	Sequence 32, Appl
586	18.8	0.4	67	10	US-09-920-342-1	Sequence 1, Appl1	659	18.6	0.4	30	10	US-09-864-761-18246	Sequence 18246, Ap
587	18.8	0.4	69	8	US-08-896-332-1	Sequence 1, Appl1	660	18.6	0.4	38	10	US-09-864-761-18246	Sequence 18246, Ap
588	18.8	0.4	70	10	US-09-815-943-545	Sequence 2939, App	661	18.6	0.4	43	10	US-09-864-761-18246	Sequence 18246, Ap
589	18.8	0.4	71	10	US-09-983-965-2929	Sequence 9, Appl1	662	18.6	0.4	43	10	US-09-864-761-18246	Sequence 18246, Ap
590	18.8	0.4	71	10	US-09-833-555-6	Sequence 9, Appl1	663	18.6	0.4	43	10	US-09-864-761-18246	Sequence 18246, Ap
591	18.8	0.4	74	10	US-09-887-384A-7	Sequence 7, Appl1	664	18.6	0.4	45	10	US-09-864-761-18246	Sequence 18246, Ap
592	18.8	0.4	74	10	US-09-887-384A-7	Sequence 7, Appl1	665	18.6	0.4	45	10	US-09-864-761-18246	Sequence 18246, Ap
593	18.8	0.4	74	10	US-09-250-611-7	Sequence 23, Appl	666	18.6	0.4	47	10	US-09-864-761-18246	Sequence 18246, Ap
594	18.8	0.4	75	10	US-09-972-599A-23	Sequence 23, Appl	667	18.6	0.4	51	10	US-09-864-761-18246	Sequence 18246, Ap
595	18.8	0.4	75	10	US-09-774-203A-3	Sequence 27825, A	668	18.6	0.4	51	10	US-09-864-761-18246	Sequence 18246, Ap
596	18.8	0.4	76	10	US-09-864-761-27825	Sequence 522, App	669	18.6	0.4	58	10	US-09-864-761-18246	Sequence 18246, Ap
597	18.8	0.4	77	10	US-09-783-590-522	Sequence 290, App	670	18.6	0.4	60	10	US-09-864-761-18246	Sequence 18246, Ap
598	18.8	0.4	77	10	US-09-783-590-522	Sequence 10, Appl	671	18.6	0.4	60	10	US-09-864-761-18246	Sequence 18246, Ap
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600	18.8	0.4	78	10	US-09-960-352-6606	Sequence 138, App	673	18.6	0.4	61	10	US-09-864-761-18246	Sequence 18246, Ap
601	18.8	0.4	79	10	US-09-777-564-1031	Sequence 1031, Ap	674	18.6	0.4	61	10	US-09-864-761-18246	Sequence 18246, Ap
602	18.8	0.4	79	10	US-09-777-564-1031	Sequence 26473, A	675	18.6	0.4	65	10	US-09-864-761-18246	Sequence 18246, Ap
603	18.8	0.4	79	10	US-09-864-761-26473	Sequence 206, App	676	18.6	0.4	66	10	US-09-864-761-18246	Sequence 18246, Ap
						Sequence 7120, Ap							

C 677	18.4	0.4	70	9	US-09-440-829-30	Sequence 30, Appl	750	18.4	0.4	99	10	US-09-922-261-280	Sequence 280, App
C 678	18.4	0.4	73	10	US-09-783-590-2555	Sequence 2555, Ap	751	18.4	0.4	100	9	US-09-933-797-773	Sequence 773, App
C 679	18.4	0.4	75	10	US-09-864-761-31308	Sequence 31308, A	C 752	18.4	0.4	100	10	US-09-770-696-904	Sequence 904, App
C 680	18.4	0.4	75	12	US-10-033-528-1825	Sequence 1825, Ap	C 753	18.4	0.4	100	10	US-09-770-696-908	Sequence 908, App
C 681	18.4	0.4	76	10	US-09-969-373-875	Sequence 875, App	C 754	18.4	0.4	100	10	US-09-864-761-18200	Sequence 18200, A
C 682	18.4	0.4	77	10	US-09-878-574-15189	Sequence 15189, A	C 755	18.4	0.4	100	10	US-09-864-761-30750	Sequence 30750, A
C 683	18.4	0.4	78	10	US-09-749-234A-12	Sequence 12, Appl	C 756	18.4	0.4	100	10	US-09-864-761-32543	Sequence 32543, A
C 684	18.4	0.4	79	10	US-09-983-965-2270	Sequence 2270, Ap	C 757	18.4	0.4	100	10	US-09-851-190A-5	Sequence 5, Appl
C 685	18.4	0.4	80	9	US-09-440-829-29	Sequence 29, Appl	C 758	18.4	0.4	100	10	US-09-764-547-1114	Sequence 1114, Ap
C 686	18.4	0.4	80	10	US-09-864-761-16921	Sequence 16921, A	C 759	18.2	0.4	27	10	US-09-758-735-6	Sequence 6, Appl
C 687	18.4	0.4	80	10	US-09-864-761-131577	Sequence 31577, A	C 760	18.2	0.4	27	10	US-09-758-735-6	Sequence 7, Appl
C 688	18.4	0.4	81	10	US-09-864-761-17801	Sequence 17801, A	C 761	18.2	0.4	28	9	US-09-942-087A-24	Sequence 24, Appl
C 689	18.4	0.4	81	10	US-09-864-761-23245	Sequence 23245, A	C 762	18.2	0.4	28	10	US-09-779-233-12	Sequence 12, Appl
C 690	18.4	0.4	81	10	US-09-983-965-3703	Sequence 3703, Ap	C 763	18.2	0.4	28	10	US-09-844-508-22	Sequence 22, Appl
C 691	18.4	0.4	82	10	US-09-294-0938-462	Sequence 462, App	C 764	18.2	0.4	38	10	US-09-843-946-6	Sequence 6, Appl
C 692	18.4	0.4	82	10	US-09-864-761-32335	Sequence 32335, A	C 765	18.2	0.4	40	10	US-09-790-417-210	Sequence 210, App
C 693	18.4	0.4	82	10	US-09-969-373-1523	Sequence 1523, Ap	C 766	18.2	0.4	43	10	US-09-774-021-1	Sequence 1, Appl
C 694	18.4	0.4	83	10	US-09-969-373-1092	Sequence 1092, Ap	C 767	18.2	0.4	50	10	US-09-223-490-19	Sequence 19, Appl
C 695	18.4	0.4	84	8	US-08-791-391A-10	Sequence 10, Appl	C 768	18.2	0.4	55	10	US-09-874-547-42	Sequence 42, Appl
C 696	18.4	0.4	84	8	US-08-791-391A-10	Sequence 10, Appl	C 769	18.2	0.4	55	10	US-09-841-132-35	Sequence 35, Appl
C 697	18.4	0.4	84	10	US-09-864-761-21796	Sequence 21796, A	C 770	18.2	0.4	55	10	US-09-841-132-35	Sequence 35, Appl
C 698	18.4	0.4	84	10	US-09-864-761-29626	Sequence 29626, A	C 771	18.2	0.4	55	10	US-09-920-300A-1151	Sequence 1151, Ap
C 699	18.4	0.4	84	10	US-09-988-598-1221	Sequence 1221, Ap	C 772	18.2	0.4	55	12	US-10-033-608-1151	Sequence 1151, Ap
C 700	18.4	0.4	85	10	US-09-864-761-19261	Sequence 19261, A	C 773	18.2	0.4	56	9	US-09-144-886-42	Sequence 42, Appl
C 701	18.4	0.4	85	10	US-09-864-761-23028	Sequence 23028, A	C 774	18.2	0.4	60	10	US-09-294-0938-3000	Sequence 3000, Ap
C 702	18.4	0.4	85	10	US-09-864-761-26472	Sequence 26472, A	C 775	18.2	0.4	60	10	US-09-865-807-62	Sequence 62, Appl
C 703	18.4	0.4	85	10	US-09-864-761-27561	Sequence 27561, A	C 776	18.2	0.4	67	10	US-10-021-121-8	Sequence 8, Appl
C 704	18.4	0.4	87	10	US-09-783-590-7183	Sequence 7183, Ap	C 777	18.2	0.4	69	10	US-09-923-876-2017	Sequence 2017, Ap
C 705	18.4	0.4	88	10	US-09-179-536B-262	Sequence 262, App	C 778	18.2	0.4	70	10	US-09-983-965-1794	Sequence 1794, Ap
C 706	18.4	0.4	88	10	US-09-864-761-19822	Sequence 19822, A	C 779	18.2	0.4	70	10	US-09-790-417-40	Sequence 40, Appl
C 707	18.4	0.4	88	10	US-09-764-847-18922	Sequence 1892, Ap	C 780	18.2	0.4	70	10	US-09-790-417-41	Sequence 41, Appl
C 708	18.4	0.4	89	10	US-09-864-761-24162	Sequence 24162, A	C 781	18.2	0.4	70	10	US-09-790-417-41	Sequence 41, Appl
C 709	18.4	0.4	89	10	US-09-864-761-31294	Sequence 31294, A	C 782	18.2	0.4	70	12	US-10-108-280-17	Sequence 14, App
C 710	18.4	0.4	89	10	US-09-783-590-3643	Sequence 3643, Ap	C 783	18.2	0.4	74	10	US-09-949-559-83	Sequence 17, Appl
C 711	18.4	0.4	89	10	US-09-764-855-329	Sequence 329, App	C 784	18.2	0.4	75	10	US-09-864-761-19270	Sequence 83, Appl
C 712	18.4	0.4	90	9	US-09-440-829-28	Sequence 28, Appl	C 785	18.2	0.4	75	10	US-09-864-761-23255	Sequence 23255, A
C 713	18.4	0.4	90	10	US-09-864-761-27853	Sequence 27853, A	C 786	18.2	0.4	75	10	US-09-864-761-26972	Sequence 26972, A
C 714	18.4	0.4	90	10	US-09-919-580-157	Sequence 157, App	C 787	18.2	0.4	77	10	US-09-878-574-10032	Sequence 10032, A
C 715	18.4	0.4	90	10	US-09-969-373-1419	Sequence 1419, Ap	C 788	18.2	0.4	77	10	US-09-864-761-18990	Sequence 18990, A
C 716	18.4	0.4	91	10	US-09-864-761-28235	Sequence 28235, A	C 789	18.2	0.4	77	10	US-09-983-965-5582	Sequence 5582, Ap
C 717	18.4	0.4	91	10	US-09-864-761-32901	Sequence 32901, A	C 790	18.2	0.4	78	10	US-09-864-761-29123	Sequence 29123, Ap
C 718	18.4	0.4	92	9	US-09-933-797-777	Sequence 777, App	C 791	18.2	0.4	79	10	US-09-864-761-28828	Sequence 28828, A
C 719	18.4	0.4	92	10	US-09-864-761-30909	Sequence 30909, A	C 792	18.2	0.4	81	10	US-09-864-761-11137	Sequence 11137, A
C 720	18.4	0.4	92	10	US-09-864-761-31063	Sequence 31063, A	C 793	18.2	0.4	81	10	US-09-783-590-11137	Sequence 11137, A
C 721	18.4	0.4	93	10	US-09-923-876-3860	Sequence 3860, Ap	C 794	18.2	0.4	83	10	US-09-974-300-41194	Sequence 29521, A
C 722	18.4	0.4	93	10	US-09-878-574-2753	Sequence 2753, Ap	C 795	18.2	0.4	83	10	US-09-864-761-29521	Sequence 27323, A
C 723	18.4	0.4	93	12	US-10-029-913-1	Sequence 1, Appl	C 796	18.2	0.4	83	10	US-09-864-761-29521	Sequence 27323, A
C 724	18.4	0.4	94	10	US-09-923-876-2143	Sequence 2143, Ap	C 797	18.2	0.4	83	10	US-09-864-761-29521	Sequence 27323, A
C 725	18.4	0.4	94	10	US-09-864-761-21968	Sequence 21968, A	C 798	18.2	0.4	83	10	US-09-864-761-29521	Sequence 27323, A
C 726	18.4	0.4	94	10	US-09-864-761-24481	Sequence 24481, A	C 799	18.2	0.4	83	10	US-09-920-300A-797	Sequence 797, App
C 727	18.4	0.4	94	10	US-09-864-761-33219	Sequence 33219, A	C 800	18.2	0.4	85	10	US-09-938-598-121	Sequence 121, App
C 728	18.4	0.4	94	10	US-09-969-373-754	Sequence 754, App	C 801	18.2	0.4	85	9	US-09-864-761-22935	Sequence 22935, A
C 729	18.4	0.4	95	10	US-09-864-761-20377	Sequence 20377, A	C 802	18.2	0.4	86	10	US-09-864-761-24779	Sequence 24779, A
C 730	18.4	0.4	95	10	US-09-864-761-20377	Sequence 20377, A	C 803	18.2	0.4	86	10	US-09-864-761-28595	Sequence 28595, A
C 731	18.4	0.4	95	10	US-09-864-761-20377	Sequence 22457, A	C 804	18.2	0.4	86	10	US-09-864-761-31082	Sequence 31082, A
C 732	18.4	0.4	95	10	US-09-864-761-22457	Sequence 22457, A	C 805	18.2	0.4	87	10	US-09-764-846-297	Sequence 297, App
C 733	18.4	0.4	95	10	US-09-728-574-46	Sequence 46, Appl	C 806	18.2	0.4	87	10	US-09-280-030-59	Sequence 59, Appl
C 734	18.4	0.4	95	10	US-09-960-352-2344	Sequence 2344, Ap	C 807	18.2	0.4	87	10	US-09-864-761-22539	Sequence 22539, A
C 735	18.4	0.4	96	10	US-09-864-761-22669	Sequence 22669, A	C 808	18.2	0.4	87	10	US-09-864-761-1896	Sequence 1896, Ap
C 736	18.4	0.4	96	10	US-09-969-373-605	Sequence 605, App	C 809	18.2	0.4	88	10	US-09-864-761-21661	Sequence 21661, A
C 737	18.4	0.4	97	10	US-09-864-761-23587	Sequence 23587, A	C 810	18.2	0.4	88	10	US-09-864-761-24747	Sequence 24747, A
C 738	18.4	0.4	97	10	US-09-864-761-30815	Sequence 30815, A	C 811	18.2	0.4	88	10	US-09-864-761-32670	Sequence 32670, A
C 739	18.4	0.4	97	10	US-09-783-590-3695	Sequence 3695, Ap	C 812	18.2	0.4	88	10	US-09-864-761-32737	Sequence 32737, A
C 740	18.4	0.4	97	10	US-09-969-373-218	Sequence 218, App	C 813	18.2	0.4	89	10	US-09-960-288-2	Sequence 2, Appl
C 741	18.4	0.4	97	10	US-09-969-373-287	Sequence 287, App	C 814	18.2	0.4	89	10	US-09-878-574-6166	Sequence 6166, Ap
C 742	18.4	0.4	97	10	US-09-915-343-838	Sequence 838, App	C 815	18.2	0.4	90	10	US-09-783-590-982	Sequence 982, App
C 743	18.4	0.4	98	10	US-09-815-343-1486	Sequence 1486, Ap	C 816	18.2	0.4	91	10	US-09-864-761-23392	Sequence 23392, A
C 744	18.4	0.4	98	10	US-09-864-761-16858	Sequence 16858, Ap	C 817	18.2	0.4	91	10	US-09-864-761-30637	Sequence 30637, A
C 745	18.4	0.4	98	10	US-09-864-761-24409	Sequence 24409, A	C 818	18.2	0.4	91	10	US-09-864-761-32737	Sequence 32737, A
C 746	18.4	0.4	98	10	US-09-864-761-29441	Sequence 29441, A	C 819	18.2	0.4	91	10	US-09-960-288-2	Sequence 2, Appl
C 747	18.4	0.4	99	10	US-09-823-876-3668	Sequence 3602, Ap	C 820	18.2	0.4	91	10	US-09-878-574-6166	Sequence 6166, Ap
C 748	18.4	0.4	99	10	US-09-815-242-2668	Sequence 2668, Ap	C 821	18.2	0.4	92	10	US-09-783-590-2773	Sequence 2773, Ap
C 749	18.4	0.4	99	10	US-09-815-242-3142	Sequence 3142, Ap	C 822	18.2	0.4	92	10	US-09-864-761-11775	Sequence 11775, A
					US-09-878-574-15431	Sequence 15431, A						US-09-864-761-21002	Sequence 21002, A



C 823	18.2	0.4	92	10	US-09-864-761-23433	Sequence 23433, A	896	18	0.4	79	12	US-10-010-742-98	Sequence 98, Appl
C 824	18.2	0.4	92	10	US-09-864-761-28380	Sequence 28380, A	897	18	0.4	80	10	US-09-783-590-11462	Sequence 11462, A
C 825	18.2	0.4	92	10	US-09-864-761-28617	Sequence 28617, A	898	18	0.4	82	10	US-09-864-761-26018	Sequence 26018, A
C 826	18.2	0.4	92	10	US-09-864-761-29479	Sequence 29479, A	C 899	18	0.4	83	10	US-09-864-761-30161	Sequence 30161, A
C 827	18.2	0.4	92	10	US-09-783-590-1375	Sequence 1375, Ap	C 900	18	0.4	83	10	US-09-812-102-56	Sequence 56, Appl
C 828	18.2	0.4	92	10	US-09-772-134B-2	Sequence 2, Appl1	C 901	18	0.4	83	10	US-10-046-935-1971	Sequence 1971, Ap
C 829	18.2	0.4	93	10	US-09-864-761-19848	Sequence 19848, A	C 902	18	0.4	84	10	US-09-923-876-1355	Sequence 1355, Ap
C 830	18.2	0.4	93	10	US-09-864-761-25858	Sequence 25858, A	C 903	18	0.4	84	10	US-09-864-761-23792	Sequence 23792, A
C 831	18.2	0.4	93	10	US-09-864-761-29240	Sequence 29240, A	C 904	18	0.4	84	10	US-09-864-761-25165	Sequence 25165, A
C 832	18.2	0.4	93	10	US-09-864-761-29324	Sequence 29324, A	C 905	18	0.4	84	10	US-09-864-761-30825	Sequence 30825, A
C 833	18.2	0.4	93	10	US-09-935-299-497	Sequence 497, Ap	C 906	18	0.4	84	10	US-09-783-590-4943	Sequence 4943, Ap
C 834	18.2	0.4	94	10	US-10-046-935-1602	Sequence 1602, Ap	C 907	18	0.4	85	10	US-09-294-093B-1591	Sequence 1591, A
C 835	18.2	0.4	94	10	US-09-864-761-11891	Sequence 31891, A	C 908	18	0.4	85	10	US-09-864-761-25654	Sequence 25654, A
C 836	18.2	0.4	94	10	US-09-878-574-10183	Sequence 10183, A	C 909	18	0.4	85	10	US-09-781-804-55	Sequence 55, Appl
C 837	18.2	0.4	95	10	US-09-864-761-11559	Sequence 31959, A	C 910	18	0.4	85	10	US-09-923-876-1618	Sequence 1618, Ap
C 838	18.2	0.4	95	10	US-09-864-761-13170	Sequence 33170, A	C 911	18	0.4	86	10	US-09-864-761-29307	Sequence 29307, A
C 839	18.2	0.4	95	10	US-09-864-761-17065	Sequence 17065, A	C 912	18	0.4	86	10	US-09-815-242-2780	Sequence 2780, Ap
C 840	18.2	0.4	96	10	US-09-864-761-29450	Sequence 29450, A	C 913	18	0.4	86	10	US-09-815-242-2892	Sequence 2892, Ap
C 841	18.2	0.4	96	10	US-09-985-965-3278	Sequence 3278, Ap	C 914	18	0.4	86	10	US-09-864-761-25661	Sequence 25661, A
C 842	18.2	0.4	96	12	US-10-078-777-8	Sequence 8, Appl1	C 915	18	0.4	87	10	US-09-864-761-32508	Sequence 32508, A
C 843	18.2	0.4	96	12	US-09-864-761-22933	Sequence 22933, A	C 916	18	0.4	87	10	US-09-864-761-32508	Sequence 32508, A
C 844	18.2	0.4	97	10	US-09-864-761-27993	Sequence 27993, A	C 917	18	0.4	87	10	US-09-864-761-32508	Sequence 32508, A
C 845	18.2	0.4	97	10	US-09-864-761-33135	Sequence 33135, A	C 918	18	0.4	87	10	US-09-864-761-32508	Sequence 32508, A
C 846	18.2	0.4	97	10	US-09-969-373-218	Sequence 218, Appl1	C 919	18	0.4	89	10	US-09-919-580-374	Sequence 374, Ap
C 847	18.2	0.4	97	10	US-09-969-373-218	Sequence 218, Appl1	C 920	18	0.4	89	10	US-09-783-590-2935	Sequence 2935, Ap
C 848	18.2	0.4	97	10	US-09-864-761-22863	Sequence 22863, A	C 921	18	0.4	90	10	US-09-853-666-25	Sequence 559, Appl
C 849	18.2	0.4	97	10	US-09-864-761-22944	Sequence 22944, A	C 922	18	0.4	90	10	US-09-864-761-18928	Sequence 18928, A
C 850	18.2	0.4	98	10	US-09-864-761-23756	Sequence 23756, A	C 923	18	0.4	90	10	US-09-864-761-29597	Sequence 29597, A
C 851	18.2	0.4	98	10	US-09-864-761-29457	Sequence 29457, A	C 924	18	0.4	90	10	US-09-137-531-10	Sequence 10, Appl
C 852	18.2	0.4	98	10	US-09-815-242-1348	Sequence 1348, Ap	C 925	18	0.4	90	10	US-09-137-531-11	Sequence 11, Appl
C 853	18.2	0.4	98	10	US-09-864-761-27787	Sequence 27787, A	C 926	18	0.4	90	10	US-09-962-055-34	Sequence 34, Appl
C 854	18.2	0.4	99	10	US-09-864-761-29555	Sequence 29555, A	C 927	18	0.4	90	10	US-09-878-574-15188	Sequence 15188, A
C 855	18.2	0.4	100	9	US-09-788-268-3	Sequence 3, Appl1	C 928	18	0.4	90	10	US-09-783-590-9712	Sequence 9712, Ap
C 856	18.2	0.4	100	9	US-09-823-876-3853	Sequence 3853, Ap	C 929	18	0.4	90	10	US-09-757-0499-46	Sequence 46, Appl
C 857	18.2	0.4	100	10	US-09-864-761-19385	Sequence 19385, A	C 930	18	0.4	90	10	US-09-912-679-33	Sequence 33, Appl
C 858	18.2	0.4	100	10	US-09-864-761-24400	Sequence 24400, A	C 931	18	0.4	90	10	US-09-822-698A-37	Sequence 37, Appl
C 859	18.2	0.4	100	10	US-09-864-761-28589	Sequence 28589, A	C 932	18	0.4	90	10	US-10-023-529-34	Sequence 34, Appl
C 860	18.2	0.4	100	10	US-09-878-574-2712	Sequence 54, Appl1	C 933	18	0.4	91	10	US-10-023-523-34	Sequence 2335, A
C 861	18.2	0.4	100	10	US-09-935-371-54	Sequence 12, Appl1	C 934	18	0.4	91	10	US-09-864-761-29335	Sequence 29335, A
C 862	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 935	18	0.4	92	10	US-09-923-876-1869	Sequence 1869, A
C 863	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 936	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 864	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 937	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 865	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 938	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 866	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 939	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 867	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 940	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 868	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 941	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 869	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 942	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 870	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 943	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 871	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 944	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 872	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 945	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 873	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 946	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 874	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 947	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 875	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 948	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 876	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 949	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 877	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 950	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 878	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 951	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 879	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 952	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 880	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 953	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 881	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 954	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 882	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 955	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 883	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 956	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 884	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 957	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 885	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 958	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 886	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 959	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 887	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 960	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 888	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 961	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 889	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 962	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 890	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 963	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 891	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 964	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 892	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 965	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 893	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 966	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 894	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 967	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A
C 895	18.2	0.4	100	10	US-09-978-285A-307	Sequence 307, Appl	C 968	18	0.4	92	10	US-09-864-761-27482	Sequence 27482, A

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C 969 18 0.4 100 US-09-864-761-28376 Sequence 28376, A
C 970 18 0.4 100 US-09-864-761-31702 Sequence 31702, A
C 971 18 0.4 100 US-09-728-446-624 Sequence 624, App
972 18 0.4 100 US-09-783-590-10893 Sequence 10893, A
973 18 0.4 100 US-09-669-373-1032 Sequence 1032, App
974 18 0.4 100 US-09-924-035A-1078 Sequence 1078, App
975 18 0.4 100 US-09-924-035A-737 Sequence 737, App
976 18 0.4 100 US-09-781-804-50 Sequence 50, App
977 18 0.4 35 US-09-882-434A-14 Sequence 14, App
978 17.8 0.4 38 US-09-096-749A-23 Sequence 23, App
979 17.8 0.4 38 US-09-851-401-35 Sequence 35, App
980 17.8 0.4 38 US-09-922-101-35 Sequence 8, App
981 17.8 0.4 38 US-10-007-448-8 Sequence 112, App
982 17.8 0.4 39 US-09-903-456-112 Sequence 14, App
C 983 17.8 0.4 40 US-09-274-163E-14 Sequence 15, App
984 17.8 0.4 44 US-10-058-820-15 Sequence 6, App
985 17.8 0.4 44 US-09-894-927A-6 Sequence 69, App
C 986 17.8 0.4 45 US-09-893-615-69 Sequence 15, App
C 987 17.8 0.4 45 US-09-965-602-15 Sequence 57, App
988 17.8 0.4 52 US-09-874-547-57 Sequence 40, App
989 17.8 0.4 56 US-09-144-886-40 Sequence 74, App
C 990 17.8 0.4 57 US-09-426-548-74 Sequence 71, App
991 17.8 0.4 61 US-09-919-580-741 Sequence 9612, App
992 17.8 0.4 64 US-09-783-590-9612 Sequence 8, App1
993 17.8 0.4 65 US-09-928-248-8 Sequence 5162, App
994 17.8 0.4 67 US-09-876-574-5162 Sequence 1837, App
C 995 17.8 0.4 68 US-09-833-381-1837 Sequence 1840, App
C 996 17.8 0.4 70 US-09-783-590-8140 Sequence 8, App1
997 17.8 0.4 72 US-09-466-320-8 Sequence 2573, App
998 17.8 0.4 74 US-09-923-876-2573 Sequence 59, App1
C 999 17.8 0.4 74 US-09-916-940-59 Sequence 59, App1
C1000 17.8 0.4 74 US-09-918-601-59 Sequence 59, App1
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## ALIGNMENTS

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RESULT 1
US-09-923-876-2711
; Sequence 2711, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (lto)
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923, 876
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 2711
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700161035H1
US-09-923-876-2711
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Query Match 0.5%; Score 26.2; DB 10; Length 90;
Best Local Similarity 56.3%; Pred. No. 7.8e+02;
Matches 49; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
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QY 3570 GAGTACCGAGAAATGAGGAAAGATATCATGCTCATGTTGATACGCTTAAGTC 3629
Db 1 GACATACCTTCGATGATTTGGACCGAGATTTCAATTTGAGAGAGTTTGTGGCCTATATC 60
QY 3630 CTATGATTAATGTTATGACGCTTGCTT 3656
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Db 61 ATTTCGGGCTGTTCTTCGACATTTGCTT 87
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RESULT 2
US-09-919-580-772/c
; Sequence 772, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 772
; LENGTH: 81
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3, 4
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-772
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Query Match 0.5%; Score 25.8; DB 10; Length 81;
Best Local Similarity 57.0%; Pred. No. 9.4e+02;
Matches 45; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
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QY 3723 CACCTCATCAGCGTCGACACCGGGAGCTGATGCCATGAAGAGATTGATTCAACC 3782
Db 79 CAGCAGAAAGCAGGTCACCTTTGGGAGCAGAGAGCCCAATTAAGTTCCAGATTCAAAA 20
QY 3783 TAATGACCTAAGACTATAC 3801
Db 19 AAAAAAAAAAAGGCGCNC 1
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RESULT 3
US-09-864-761-31768/c
; Sequence 31768, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aemica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; LENGTH: 91
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007684.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EST HUMAN HIT: A1273296.1, EVALUE 3.00e-44
; OTHER INFORMATION: NT HIT: G14506376, EVALUE 2.00e-44
; OTHER INFORMATION: SWISSPROT HIT: P41892, EVALUE 2.40e-02
; US-09-664-761-31768

Query Match      0.5%; Score 25; DB 10; Length 91;
Best Local Similarity 61.5%; Pred. No. 1.7e+03;
Matches 40; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 3815 ACGAATGAAATATTCGAGCGCATCAACACCCCATCGTGTGCTTTGTTGGTGG 3874
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 67 AAGCAATTAATATGATGAAGACGTGAACACCCCAATATGTTGCTTATTTGGAAGCT 8
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3875 AGCTC 3879
    ||| |||
DB 7 ATCTC 3

RESULT 4
US-09-733-692A-31/C
; Sequence 31, Application US/09733692A
; GENERAL INFORMATION:
; APPLICANT: Murphy, Brian R.
; APPLICANT: Collins, Peter L.
; APPLICANT: Schmidt, Alexander C.
; APPLICANT: Durbin, Anna P.
; APPLICANT: Skidopoulos, Mario H.
; APPLICANT: Tao, Tao
; TITLE OF INVENTION: USE OF RECOMBINANT PARAINFLUENZA VIRUSES (PIVs) AS
; TITLE OF INVENTION: VECTORS TO PROTECT AGAINST INFECTION AND DISEASE CAUSED
; FILE REFERENCE: 15280-404100US
; CURRENT APPLICATION NUMBER: US/09/733,692A
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/170,195
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 31
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Reverse primer

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; OTHER INFORMATION: for RSV A G gene insert
US-09-733-692A-31
Query Match      0.5%; Score 24.8; DB 9; Length 92;
Best Local Similarity 63.3%; Pred. No. 2e+03; 22; Indels 0; Gaps 0;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 45 TTACTCTCCCCCGACGACAGTGAACGATGTCAACCAACATCAGAGGAA 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 80 TTACTCTCCACCCACACACACGACGAGTGAATAAAGTAAGAAAAAATTAGATTAA 21

RESULT 5
US-09-664-761-20908/C
; Sequence 20908, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20908
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009305.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.8

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OTHER INFORMATION: NT HIT: AJ271735.1, EVALUE 1.80e-01  
OTHER INFORMATION: EST\_HUMAN HIT: AI444613.1, EVALUE 8.50e-01  
OTHER INFORMATION: SWISSPROT HIT: Q01851, EVALUE 9.20e+00  
US-09-864-761-20908

Query Match  
Best Local Similarity 0.5%; Score 24.4; DB 10; Length 99;  
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 751 AATGACTTCTAGAGAGGCGATCGACCTCTGGAACAAGATTGAGTTAC 810  
DB 94 AATATGATGCGCTAGCATGATGATCCAGCCCTGCGCAGACCAATGATGATCTTC 35  
QY 811 TCACACATATATCA 824  
DB 34 TGACCTCATCATCA 21

RESULT 6  
US-09-864-761-28769/c  
Sequence 28769, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 28769  
LENGTH: 80  
TYPE: DNA

ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AL121582.14  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.85  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.88  
OTHER INFORMATION: EST\_HUMAN HIT: BF475330.1, EVALUE 9.50e-01  
US-09-864-761-28769

Query Match  
Best Local Similarity 0.5%; Score 24.2; DB 10; Length 80;  
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 3462 AAGAGACTTGGGACCTTCGACACTAATCAGCCAGAGTAAGATTGCTTAACACT 3521  
DB 66 AAGAAATTTATCAGACCTGTGACATTTAAAGCCACAGAAATATCTCTGTTAAATT 7  
QY 3522 A 3522  
DB 6 A 6

RESULT 7  
US-09-864-761-28328/c  
Sequence 28328, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
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PRIOR FILING DATE: 2001-01-30  
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PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30

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PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 25222
LENGTH: 99
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009013.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.7
OTHER INFORMATION: EST_HUMAN HIT: BF304683.1, EVALUE 4.00e-28
OTHER INFORMATION: SWISSPROT HIT: Q89940, EVALUE 5.50e+00
OTHER INFORMATION: NT HIT: AL163210.2, EVALUE 5.00e-30
US-09-864-761-25222

Query Match          0.5%; Score 24.2; DB 10; Length 99;
Best Local Similarity 66.0%; Pred. No. 3.2e+03;
Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY      924 GAAGGACTATGAATAAAATATGTCTGCACAAGAAGACTTCAGAGCAGGGTGCGAGGCAC 976
Db       10 GAATGACTTTGCACAAAATGCTGATGTGATGATGATTAATTAAGCTCCAGAGCAC 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
US-09-847-113-6
Sequence 6, Application US/09847113
Patent No. US2002012134A1
GENERAL INFORMATION:
APPLICANT: Yu Changjun
TITLE OR INVENTION: Target Analyte Detection Using Asymmetrical Self-Assembled Monolayers
FILE REFERENCE: A-693065-1
CURRENT FILING DATE: 2001/09/04/7, 113
PRIOR APPLICATION NUMBER: US/09/847, 113
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/626, 096
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 86
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sandwich assay target and signaling probe.
US-09-847-113-6

Query Match          0.5%; Score 23.8; DB 10; Length 86;
Best Local Similarity 59.7%; Pred. No. 3.7e+03;
Matches 40; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY      3871 GTGGAGCTCCATCAAGAGAAATGTACATCTTCAATGAGAGTAGTGGCATGAGGGAGCTTTA 3930
Db        5 GTGGGGGGGACATCAAGCAGCAGCCATGCAATGTTTAAAGAGACCATCAATGAGAGAGCTGCA 64
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 65 GAATGGG 71

## RESULT 10

US-09-864-761-22288

; Sequence 22288, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; FILE REFERENCE: Acomica-x-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 22288

; LENGTH: 90

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC004613.1

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

; OTHER INFORMATION: EST\_HUMAN HTT: Z36771.1, EVALUATE 1.80e-02

; OTHER INFORMATION: NT HTT: D78589.1, EVALUATE 1.20e-02

; US-09-864-761-22288

Query Match 0.5%; Score 23.8; DB 10; Length 90;  
Best Local Similarity 62.7%; Pred. No. 3.8e+03;  
Matches 37; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1106 AAGTATATGACCGGAGTATGAGGTGATGACACAGAGAGGAATTAAAGAGTTGGAA 1164

Db 20 AGGCAATATATCAGAGCAAAAGCAAGAGGCAAGAGAGCAAAAACAGAGGAGGAA 78

## RESULT 11

US-09-969-373-453

; Sequence 453, Application US/09969373

; Patent No. US20020133852A1

; GENERAL INFORMATION:

; APPLICANT: Efferetz, Roger J.

; APPLICANT: Hauge, Brian M.

; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

; FILE REFERENCE: 38-10(52679)A

; CURRENT APPLICATION NUMBER: US/09/969,373

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US 09/754,853

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: US 09/760,427

; PRIOR FILING DATE: 2001-01-13

; PRIOR APPLICATION NUMBER: US 09/855,768

; PRIOR FILING DATE: 2001-05-15

; NUMBER OF SEQ ID NOS: 4593

; SEQ ID NO 453

; LENGTH: 100

; TYPE: DNA

; ORGANISM: Glycine max

; US-09-969-373-453

Query Match 0.5%; Score 23.8; DB 10; Length 100;  
Best Local Similarity 72.1%; Pred. No. 4.1e+03;  
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 188 AAACAGTGGAGATGTGGAATATACACTATTAACAGAGAA 230

Db 29 AAGAAGTGTATTATGAGAGAAAGAAAGCAAGCAAGCAAGAA 71

## RESULT 12

US-09-998-598-1313/c

; Sequence 1313, Application US/09998598

; Patent No. US20020150922A1

; GENERAL INFORMATION:

; APPLICANT: Stolk, John A.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Meagher, Madelein Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.561

; CURRENT APPLICATION NUMBER: US/09/998,598

; PRIOR FILING DATE: 2001-11-16

; NUMBER OF SEQ ID NOS: 2606

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 1313

; LENGTH: 79

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-998-598-1313

Query Match 0.5%; Score 23.6; DB 10; Length 79;  
Best Local Similarity 57.6%; Pred. No. 4e+03;  
Matches 38; Conservative 2; Mismatches 26; Indels 0; Gaps 0;

QY 3629 CCTATGATATGATATGACAGTTGGCTTGAGAGAGTGAACCTTCAATGCAAGAGGAA 3688

Db 68 CCTCAAAATATGATTATATCATAGTGAATTAAGAAGTAACGCAACCAAAAAA 9

QY 3689 ACAAAA 3694



```

; Sequence 9597, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9597
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-9597

```

```

Query Match          0.5%; Score 23.2; DB 10; Length 89;
Best Local Similarity 64.2%; Pred. No. 5.7e+03;
Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

```

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QY 1967 AATCTGTTAGAGAAAGTGAATTTACCAAGAAATACTGATTACATA 2019
Db 81 AGAATCTGCTGGAAAAAATMAAATAATAATAATAATAATAATAATA 29

```

```

RESULT 17
US-09-864-761-20158
; Sequence 20158, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20158
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL109615.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.6
; OTHER INFORMATION: EST_HUMAN HIT: BE973335.1, EVALUATE 1.10e+00
; OTHER INFORMATION: SWISSPROT HIT: 054828, EVALUATE 7.00e+00
; OTHER INFORMATION: NT HIT: 294043.1, EVALUATE 7.70e-01
US-09-864-761-20158

```

```

Query Match          0.5%; Score 23.2; DB 10; Length 93;
Best Local Similarity 61.7%; Pred. No. 5.8e+03;
Matches 37; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

```

```

QY 2496 CTATCTGCTTGCACCAAGCAGCGTGCAGCCCGTATTCAGAGCAGCTGGGGCAC 2555
Db 15 CTGCTGTTGGGGCCCAAGCAGCAGGAGCAGGAGCGATCTGGGATCAAGGGGGCAC 74

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RESULT 18
US-09-933-797-749/C
; Sequence 749, Application US/09933797
; Patent No. US2002015119A1
; GENERAL INFORMATION:
; APPLICANT: Robert A. Sikes et al.
; TITLE OF INVENTION: Isolation and Use of Fetal Urogenital
; FILE REFERENCE: 9901-007-999
; CURRENT APPLICATION NUMBER: US/09/933,797
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US/09/482,933
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: PCT/US99/10746
; PRIOR FILING DATE: 1999-05/14
; PRIOR APPLICATION NUMBER: 60/085,383
; PRIOR FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 811
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 749
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Murine
US-09-933-797-749

```

```

Query Match          0.5%; Score 23.2; DB 9; Length 94;
Best Local Similarity 53.7%; Pred. No. 5.9e+03;

```





ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC011449.3  
OTHER INFORMATION: EXPRESSED IN BONE MARROW; SIGNAL = 2.5

CURRENT APPLICATION NUMBER: US/09/864,761  
 PRIOR APPLICATION NUMBER: 2001-05-23  
 PRIOR FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00662  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00661  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00670  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: US 60/234,687  
 PRIOR FILING DATE: 2000-09-21  
 PRIOR APPLICATION NUMBER: US 09/608,408  
 PRIOR FILING DATE: 2000-06-30  
 PRIOR APPLICATION NUMBER: US 09/774,203



CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00669  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00665  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00668  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00663  
 PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US/09/864,761  
 CURRENT FILING DATE: 2001-05-23  
 PRIOR APPLICATION NUMBER: US 60/180,312  
 PRIOR FILING DATE: 2000-02-04  
 PRIOR APPLICATION NUMBER: US 60/207,456  
 PRIOR FILING DATE: 2000-05-26  
 PRIOR APPLICATION NUMBER: US 09/632,366  
 PRIOR FILING DATE: 2000-08-03  
 PRIOR APPLICATION NUMBER: GB 24263.6  
 PRIOR FILING DATE: 2000-10-04  
 PRIOR APPLICATION NUMBER: US 60/236,359  
 PRIOR FILING DATE: 2000-09-27  
 PRIOR APPLICATION NUMBER: PCT/US01/00666  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00667  
 PRIOR FILING DATE: 2001-01-30  
 PRIOR APPLICATION NUMBER: PCT/US01/00664  
 PRIOR FILING DATE: 2001-01-30

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PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31482
LENGTH: 87
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007567.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 1.2
OTHER INFORMATION: NT HIT: AL163303.2, EVALUATE 1.00e-05
OTHER INFORMATION: EST HUMAN HIT: BE221737.1, EVALUATE 1.00e-03
OTHER INFORMATION: SWISSPROT HIT: P13186, EVALUATE 1.10e+00
US-09-864-761-31482

Query Match
Best Local Similarity 62.1%; Score 22.8; DB 10; Length 87;
Matches 36; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 3215 GTTTCACCTTGGCATCGACGAGCCCGCTCATGAGCGTACCTGATGCCA 3272
DB 60 GTTTCACCTTGGCGCTTGTGATATGATGCTTGTGATGAGCTAGTGTAGACCA 3

RESULT 27
US-09-864-761-32824/c
Sequence 32824, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmca-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIORITY FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30

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PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32824
LENGTH: 89
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL030997.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.93
OTHER INFORMATION: NT HIT: M96655.1, EVALUATE 1.80e-01
US-09-864-761-32824

Query Match
Best Local Similarity 56.8%; Score 22.8; DB 10; Length 89;
Matches 42; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1981 GAGAGTGGATTTCCACCAAGAAATATCATCTAGCGGAGAGAGACGACGAGCC 2040
DB 86 GGAGAGTGGATTTCCACCAAGAAATATCATCTAGCGGAGAGAGACGACGAGCC 27

QY 2041 GCGAGCTTTTCTG 2054
DB 26 CCTAGACTTATCTG 13

RESULT 28
US-09-923-876-1300
Sequence 1300, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (lto)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
PRIORITY FILING DATE: 2001-08-06
PRIORITY APPLICATION NUMBER: 09/298,329
PRIORITY FILING DATE: 1999-04-21
PRIORITY APPLICATION NUMBER: 60/085,331
PRIORITY FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 1300
LENGTH: 98
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc-feature

```

OTHER INFORMATION: Inocyte ID No. US20020013958A1 700158456H1  
NAME/KEY: unsure  
LOCATION: 93  
OTHER INFORMATION: a, t, c, g, or other  
US-09-923-876-1300

Query Match  
Best Local Similarity 0.58; Score 22.8; DB 10; Length 98;  
Matches 45; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY 1102 TCCAAAGCTAATGAGCCGATGATGAGGTGATGACACAGAGAGATTAAAGAGCTTG 1161

DB 12 TACACAGTACTGCTGCTGGGCAATTGAGACCATACAGAGAGATTGAGAGAGCTT 71

OY 1162 GAAAGTACTACGATGAGAGAGTGA 1184

DB 72 AAAAGCTACACGACGAGAGAGCNA 94

## RESULT 29

US-09-919-580-637/c  
Sequence 637, Application US/09919580

Patent No. US20020110832A1

GENERAL INFORMATION:

APPLICANT: Pyle, Ruth

APPLICANT: Xu, Jiangchun

APPLICANT: Serist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.552

CURRENT APPLICATION NUMBER: US/09/919,580

CURRENT FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 637

LENGTH: 64

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: 56

OTHER INFORMATION: n = A,T,C or G

US-09-919-580-637

Query Match  
Best Local Similarity 0.58; Score 22.6; DB 10; Length 64;  
Matches 37; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

OY 498 AAAGCTTACCTCAGTCTCAAGAAAAAGACGAGCAAGAGAGCAAGAATACTAGCTC 557

DB 64 AAGGCTTTTCTCTTTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGGCG 5

OY 558 TG 559

DB 4 GC 3

## RESULT 30

US-09-878-574-7267/c

Sequence 7267, Application US/09878574

Patent No. US20020110548A1

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 7267  
LENGTH: 96  
TYPE: DNA  
ORGANISM: Glycine max  
OTHER INFORMATION: Clone ID: 701099674H1  
US-09-878-574-7267

Query Match  
Best Local Similarity 0.58; Score 22.6; DB 10; Length 96;  
Matches 46; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

OY 4533 TACATAAAGACTGCTGAGAGAGATTAAGCCTTTTAACCTCCAGACTGAAGCT 4592

DB 86 TACGTGATGTTGCTGAGAGAGACTGAGAGAGAGTTTGCAGACTGCAGATTCATAATTAT 27

OY 4593 GCACAGGTGACAGCGTCACTTTC 4617

DB 26 GCAGAGGGGAAACGCTTCACGCTTC 2

## RESULT 31

US-09-864-761-24215

Sequence 24215, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 24215

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? LENGTH: 98
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AL096863.10
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.87
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
US-09-864-761-24215

Query Match
Best Local Similarity 58.0%; Score 22.6; DB 10; Length 98;
Matches 40; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 956 TCCAGACAGGCTGCGACGCTCTGTTGTTAAACATCACAAGACTTAATCAGA 1015
Db 7 TTCTGGACAAATTTGAAGTACTATGTTGATTTGAAAAATTAACAGGTCTTCTCAT 66

QY 1016 AATTAGA 1024
Db 67 CACTACTGA 75

RESULT 32
US-09-864-761-25667
; Sequence 25667, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmics-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
```

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Snpmax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 25667
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005300.10
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EST HUMAN HIT: BEL59343.1, EVALUATE 1.00e-49
; OTHER INFORMATION: SWISSPROT HIT: P04468, EVALUATE 5.50e+00
US-09-864-761-25667

Query Match
Best Local Similarity 58.0%; Score 22.6; DB 10; Length 100;
Matches 40; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 3242 GCGCCGCTGCTATGAGGTACTGATGCCATAGTGCCTCTAACCACGCTATTA 3301
Db 26 GCGCTCCACCTCTGCATGCTCTCCATGCCCATGCCCTCCAGATCCAGCACTGG 85

QY 3302 TCCGCACTC 3310
Db 86 TCCACACTC 94

RESULT 33
US-09-878-574-14838
; Sequence 14838, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO: 14838
; LENGTH: 83
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701069318H1
US-09-878-574-14838

Query Match
Best Local Similarity 59.4%; Score 22.4; DB 10; Length 83;
Matches 38; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 3177 TGGCCATGTCATAGGAACACACAGTCTGTACAGGTTTGACTTCCCATTCATCG 3236
Db 6 TGGTCTGTGCGGAGCAAAACCAAGCATCTCACTTGTCTGTCCAGACATGCTCT 65

QY 3237 GAAC 3240
Db 66 GATC 69
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RESULT 34

```

US-09-864-761-19403
; Sequence 19403, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US/01-05-23
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19403
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL18555.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: O61101, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: BE929768.1, SIGNAL = 3.00e-12
; OTHER INFORMATION: NT HIT: g111434604, SIGNAL = 9.00e-47
US-09-864-761-19403

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Query Match

Best Local Similarity 62.38; Score 22.4; DB 10; Length 95;

Matches 35; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Oy 1025 TTATGGCAGTGTTCGATCATCATTTATCAGACATTCGTCGCGAGTGT 1080
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 33 TTATGGCAGTGTTCGTCGTAGACATTTATCCGAAACAGATTACAAATATTT 88

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RESULT 35

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US-09-864-761-27595/c
; Sequence 27595, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27595
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005666.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

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OTHER INFORMATION: SWISSPROT HIT: 043236, EVALUE 1.00e-12  
OTHER INFORMATION: NT HIT: U88870.1, EVALUE 1.00e-49  
OTHER INFORMATION: EST\_HUMAN HIT: AN964640.1, EVALUE 1.00e-49  
US-09-864-761-27393

Query Match 0.4%; Score 22.4; DB 10; Length 100;  
Best Local Similarity 66.7%; Pred. No. 1e+04; Mismatches 16; Indels 0; Gaps 0;  
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2566 CAGCCTGTCAAGTCCTCAGTGTGAGACCTGTGACACCTGAGA 2613  
DB 60 CAGCGGTCACATCTGCTATCTGCTTAAGCAGACACTGACA 13

RESULT 36  
US-09-864-761-24218/c  
Sequence 24218, Application US/09864761  
GENERAL INFORMATION:  
PATENT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 24218  
LENGTH: 75  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE: MAP TO AC013746.4  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7  
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 5.8  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8  
US-09-864-761-24218

Query Match 0.4%; Score 22.2; DB 10; Length 75;  
Best Local Similarity 69.8%; Pred. No. 9.7e+03; Mismatches 13; Indels 0; Gaps 0;  
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 193 GTGAGATGTGAGCAATATACCTTAAGCAGCAAGAAAGA 235  
DB 73 GAGGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 31

RESULT 37  
US-09-969-373-613/c  
Sequence 613, Application US/09969373  
PATENT: US20020133852A1  
GENERAL INFORMATION:  
PATENT: Effertz, Roger J.  
APPLICANT: Hauge, Brian M.  
APPLICANT: Hauge, Brian M.  
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
FILE REFERENCE: 38-10(52679)A  
CURRENT APPLICATION NUMBER: US/09/969,373  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US 09/754,853  
PRIOR FILING DATE: 2001-01-05  
PRIOR APPLICATION NUMBER: US 09/760,427  
PRIOR FILING DATE: 2001-01-13  
PRIOR APPLICATION NUMBER: US 09/855,768  
PRIOR FILING DATE: 2001-05-15  
NUMBER OF SEQ ID NOS: 4593  
SEQ ID NO 613  
LENGTH: 80  
TYPE: DNA  
ORGANISM: Glycine max  
US-09-969-373-613

Query Match 0.4%; Score 22.2; DB 10; Length 80;  
Best Local Similarity 56.0%; Pred. No. 1e+04; Mismatches 33; Indels 0; Gaps 0;  
Matches 42; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 4036 GACATTAAGGTCGCAATATCTTACCTCATCTGATTAATCAAACTGGAGATT 4095  
DB 76 GAAATTTAACCATCAATATATTATTATTATTATTAAATAATTTGTTCTTA 17  
QY 4096 GGATGTCAGTAAG 4110  
DB 16 TGATATTATTATTCAGC 2

RESULT 38  
US-09-864-761-22604  
Sequence 22604, Application US/09864761  
PATENT: US20020048763A1  
GENERAL INFORMATION:  
PATENT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 24218  
LENGTH: 75  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE: MAP TO AC013746.4  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8

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Query Match      0.4%: Score 22.2: DB 10: Length 83:
Best Local Similarity 64.7%: Pred. No.1e+04;
Matches 33: Conservative 0: Mismatches 18: Indels 0: Gaps 0;

QY    1106 AAGTAATGACCGCAGTATGAGGTGATGACACAGAAGAGAAATTAAAG 1156
       | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     10 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
       | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 39
US-09-878-574-5668
: Sequence 5668, Application US/09878574
: Patent No. US20020110548A1
: GENERAL INFORMATION:
: APPLICANT: Byrum, Joseph R.
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Thompson, Michael D.
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(15401)B
: CURRENT APPLICATION NUMBER: US/09/878, 574

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Query Match	0.48;	Score 22.2;	DB 10;	Length 86;
Best Local Similarity	64.7%;	Pred. No. 1.1e+04;		
Matches 33; Conservative	0;	Mismatches 18;	Indels 0;	Gaps 0;

RESULT 40  
US-09-191

1 APPLICANT: Perrin, Marilyn H.  
2  
3 APPLICANT: Chen, Kuoping  
4  
5 APPLICANT: Lewis, Kathy A.  
6  
7 APPLICANT: Vale Jr., Wyle W.  
8  
9 APPLICANT: Donaldson, Cynthia J.  
10  
11 APPLICANT: Sawchenko, Paul  
12  
13 TITLE OF INVENTION: Cloning and Recombinant Production of  
14  
15 TITLE OF INVENTION: CRF Receptor(s)  
16  
17 FIVE REFERENCE: Salviata

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? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(87)
? OTHER INFORMATION: CRR-R splice variant insert fragment
? SS-09-191-724-3

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Query Match      0.48;   Score 22.2;   DB 10;   Length 87;
Best Local Similarity 61.0%;   Pred. No. 1.1e+04;
Matches 36;   Conservative 0;   Mismatches 23;   Indels 0;   Gaps 0;

4620  GCTGCTCTGTTTCTGATGATGTCACAAAGCCCTCTGGAGGAGCTGGTGCACGAGGT 4678
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
5  GCTGACCCCAATTGGGGGAGACCAAGCAATGATGAGCCCTGGAGGAGGGGGGGCTTCATGAGT 63

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Search completed: November 11, 2002, 12:43:10
Job time : 136 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 07:02:01 ; Search time 4213 Seconds  
(without alignments)  
19182.407 Million cell updates/sec

Title: US-09-676-436-3

Sequence: 1 ctgaagaacttcctcgaatga.....ggttattttagaagaatc 4990

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 357786

Minimum DB seq length: 8  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1000 summaries

Database :  
1: em\_estba:\*  
2: em\_estlun:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estlun:\*  
6: em\_estlun:\*  
7: em\_estlun:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_hlc:\*  
11: gb\_hlc:\*  
12: gb\_estl:\*  
13: gb\_estl:\*  
14: gb\_estl:\*  
15: em\_estfun:\*  
16: em\_estfun:\*  
17: gb\_gss:\*  
18: em\_gss\_lun:\*  
19: em\_gss\_lun:\*  
20: em\_gss\_lun:\*  
21: em\_gss\_lun:\*  
22: em\_gss\_lun:\*  
23: em\_gss\_lun:\*  
24: em\_gss\_lun:\*  
25: em\_gss\_lun:\*  
26: em\_gss\_lun:\*  
27: em\_gss\_lun:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.8	0.8	95	AA990067	AA990067 ua58f02.r
2	30	0.6	64	17 DR12A12S	AL743114 Dapio rer
3	29	0.6	70	AA490364	AA490364 aa44c10.r
4	28.6	0.6	71	AT167078	AT167078 w192507.x
5	28	0.6	83	13 BU063432	BU063432 BU063432
6	27.8	0.6	65	17 BH863389	BH863389 SALK_0937

7	27.8	0.6	83	9	AI360096	AI360096 qy89d09.x
8	27.8	0.6	94	13	BI322285	BI322285 K19a08.r
9	27.8	0.6	100	9	AI154655	AI154655 mq61c08.r
10	27.4	0.5	91	14	T85845	T85845 yd61d10.r1
11	27.4	0.5	98	9	AI054386	AI054386 q17e03.x
12	26.8	0.5	88	9	AU254337	AU254337 AU254337
13	26.8	0.5	90	17	AL760836	AL760836 Arabidops
14	26.8	0.5	98	10	AV960997	AV960997 AV960997
15	26.8	0.5	100	14	C53310	C53310 C53310 Yu11
16	26.6	0.5	81	12	BE573242	BE573242 601331339
17	26.6	0.5	82	12	BF101686	BF101686 601753418
18	26.4	0.5	87	9	AA267457	AA267457 mz90a03.r
19	26.4	0.5	95	9	AA946634	AA946634 Cq38f11.s
20	26.4	0.5	95	14	R93104	R93104 EST000038.S
21	26.2	0.5	78	14	R40354	R40354 YF81d05.s1
22	26.2	0.5	93	14	AV551027	AV551027 AV551027
23	26.2	0.5	93	14	T62011	T62011 YP97B12.r1
24	26.2	0.5	78	13	BI858071	BI858071 603384887
25	26.2	0.5	85	17	BI8572076	BI8572076 G-10924.f
26	26	0.5	88	9	AA867446	AA867446 Oh41h1.s
27	26	0.5	88	17	AL757179	AL757179 Arabidops
28	26	0.5	98	17	AI251245	AI251245 qv55q12.x
29	25.8	0.5	78	9	AI035450	AI035450 db47b05.x
30	25.8	0.5	83	9	AA915897	AA915897 Oh86b08.s
31	25.8	0.5	91	9	AI340694	AI340694 LB33c02.x
32	25.8	0.5	91	9	AI894187	AI894187 mc67e06.x
33	25.8	0.5	100	9	AL794139	AL794139 AL794139
34	25.6	0.5	73	9	AI142956	AI142956 o258d01.x
35	25.6	0.5	85	9	AI086378	AI086378 o244c01.x
36	25.6	0.5	86	10	AV532477	AV532477 AV532477
37	25.6	0.5	87	17	AL754956	AL754956 Arabidops
38	25.4	0.5	79	10	AW149995	AW149995 xg32c06.x
39	25.4	0.5	89	17	AZ961698	AZ961698 2M0230B17
40	25.4	0.5	91	14	D19910	D19910 HMG5000867
41	25.4	0.5	92	17	AF149669	AF149669 AF149669
42	25.4	0.5	93	9	AA669624	AA669624 ac20a02.s
43	25.4	0.5	94	9	AL662095	AL662095 AL662095
44	25.4	0.5	94	14	B0836143	B0836143 rf42d06.y
45	25.4	0.5	95	12	AA576542	AA576542 nm66c06.s
46	25.4	0.5	99	12	BR0562479	BR0562479 gb73a06.y
47	25.4	0.5	99	12	BR0546770	BR0546770 7169e05.y
48	25.2	0.5	64	10	AW624720	AW624720 SMOVAFCAP
49	25.2	0.5	68	17	A2574215	A2574215 326PVB08
50	25.2	0.5	81	9	AA451873	AA451873 xz16e01.s
51	25.2	0.5	88	9	AI339161	AI339161 qf14p01.x
52	25.2	0.5	88	14	C01741	C01741 HMG5000363
53	25.2	0.5	94	13	BI943038	BI943038 sn03b04.y
54	25.2	0.5	97	17	TA330B01P	TA330B01P
55	25.2	0.5	98	14	NS0007	NS0007 yv24e01.r1
56	25	0.5	85	9	AI113686	AI113686 A3F Pyroc
57	25	0.5	86	9	AI539785	AI539785 fp77g05.x
58	25	0.5	90	9	AA831863	AA831863 oa59e04.s
59	25	0.5	100	9	AI080943	AI080943 BSHMFS21
60	25	0.5	78	9	H28412	H28412 y031f04.s1
61	24.8	0.5	100	14	AA922381	AA922381 Oh91d11.s
62	24.8	0.5	82	9	AA888326	AA888326 nw73b04.s
63	24.8	0.5	82	12	BF533682	BF533682 602074086
64	24.8	0.5	93	9	AA907284	AA907284 AU007284
65	24.8	0.5	97	17	A2975978	A2975978 2M0251D16
66	24.8	0.5	98	14	BO742382	BO742382 seq42f04.
67	24.8	0.5	100	17	AL764745	AL764745 Arabidops
68	24.6	0.5	68	14	BO528639	BO528639 NISC.nc07
69	24.6	0.5	92	9	AU267970	AU267970 AUD67570
70	24.6	0.5	79	9	AA984185	AA984185 am82a09.s
71	24.6	0.5	98	10	AV737113	AV737113 AV737113
72	24.6	0.5	98	17	AA7479591	AA7479591 LM0300A20
73	24.6	0.5	100	13	BI052812	BI052812 RC4-GN033
74	24.6	0.5	100	14	BO394597	BO394597 NISC-ng10
75	24.4	0.5	68	17	CNS01Y5F	AL175572 Tetradon
76	24.4	0.5	76	13	BM530543	BM530543 IKS4N07.y
77	24.4	0.5	75	17	AA611518	AA611518 LM0437G19
78	24.4	0.5	76	17	AA922726	AA922726 o184a12.s
79	24.4	0.5	95	12	BG256984	BG256984 602370A87

C 80	24.4	0.5	96	9	A1560569	A1560569 tq49b11.x	C 153	23.6	0.5	94	17	CNS033NU	AL226360 Telradon
C 81	24.4	0.5	99	12	BR361342	BR361342 ONV-PT001	C 154	23.6	0.5	96	14	BQ381729	BQ381729 K45609.Y
C 82	24.4	0.5	100	9	A1152569	A1152569 u089a03.r	C 155	23.6	0.5	97	17	A2366275	A2366275 1M01151b
C 83	24.4	0.5	100	9	A1681367	A1681367 lx46a05.x	C 156	23.6	0.5	97	9	A1864531	A1864531 w15a05.x
C 84	24.4	0.5	100	9	A1736172	A1736172 sb24c01.y	C 157	23.6	0.5	98	17	BH866271	BH866271 SALK_1009
C 85	24.4	0.5	100	9	AA623836	AA623836 vq69g02.s	C 158	23.6	0.5	98	17	CNS00XCA	AL094696 Arabidops
C 86	24.2	0.5	65	13	BJ051122	BJ051122 BM051122	C 159	23.6	0.5	99	17	A2863592	A2863592 2M0171H09
C 87	24.2	0.5	67	9	A1222915	A1222915 gm29g05.x	C 160	23.6	0.5	100	9	AA855184	AA855184 a153b12.s
C 88	24.2	0.5	78	12	BP238743	BP238743 601904328	C 161	23.6	0.5	100	9	A1499211	A1499211 t08e008.x
C 89	24.2	0.5	80	9	A1312379	A1312379 ca21c03.x	C 162	23.6	0.5	99	9	AU271250	AU271250 AU271250
C 90	24.2	0.5	83	9	A1611595	A1611595 t66f03.x	C 163	23.4	0.5	59	9	A1671994	A1671994 w02c06.x
C 91	24.2	0.5	84	10	AM675386	AM675386 bd45g09.y	C 164	23.4	0.5	73	9	A1610168	A2700117 2M0038022
C 92	24.2	0.5	93	9	A1960759	A1960759 sc90a09.y	C 165	23.4	0.5	70	9	A1610168	A1610168 tpi3h08.x
C 93	24.2	0.5	93	9	AA411602	AA411602 zvl6g05.r	C 166	23.4	0.5	76	9	A1197096	A1197096 u057d05.r
C 94	24.2	0.5	94	9	AA872482	AA872482 c110b07.s	C 167	23.4	0.5	77	9	AA789172	AA789172 ag58b09.s
C 95	24.2	0.5	94	9	A1397040	A1397040 fd25e03.y	C 168	23.4	0.5	17	AL768904	AL768904 Arabidops	
C 96	24.2	0.5	94	9	A1611586	A1611586 t16e04.x	C 169	23.4	0.5	80	14	BQ758288	BQ758288 ERMA03.SO
C 97	24.2	0.5	95	10	AV674632	AV674632 AV674632	C 170	23.4	0.5	81	14	C00156	C00156 HUMGS000579
C 98	24.2	0.5	96	10	BE246632	BE246632 NF020B02L	C 171	23.4	0.5	84	13	BM435847	BM435847 IRU544.ab
C 99	24.2	0.5	97	10	AM278082	AM278082 sf39e03.y	C 172	23.4	0.5	85	13	AA737424	AA737424 o04d008.s
C 100	24.2	0.5	98	9	A1308454	A1308454 t044a10.x	C 173	23.4	0.5	85	13	BQ7080960	BQ7080960 BQ7080960
C 101	24.2	0.5	98	9	A1540247	A1540247 t055b12.x	C 174	23.4	0.5	86	14	T82435	T82435 yc02f04.s1
C 102	24.2	0.5	99	9	A1331232	A1331232 fa98c01.y	C 175	23.4	0.5	87	9	AA546841	AA546841 vk67p02.s
C 103	24.2	0.5	56	17	B03428	B03428 CSR-179A8	C 176	23.4	0.5	87	13	B1496678	B1496678 df137c08.
C 104	24.2	0.5	74	10	AV525712	AV525712 AV525712	C 177	23.4	0.5	89	10	AM302090	AM302090 x153d11.x
C 105	24.2	0.5	75	9	A1446279	A1446279 t131d11.x	C 178	23.4	0.5	90	17	BH216218	BH216218 1006041C0
C 106	24.2	0.5	81	17	BH849361	BH849361 SALK_0695	C 179	23.4	0.5	93	9	A1428297	A1428297 mm44g08.x
C 107	24.2	0.5	84	9	AA743463	AA743463 ny19c10.s	C 180	23.4	0.5	94	10	BE032377	BE032377 sm81a11.y
C 108	24.2	0.5	87	10	AV519819	AV519819 AV519819	C 181	23.4	0.5	95	9	A1142414	A1142414 q964h04.r
C 109	24.2	0.5	88	10	AV839096	AV839096 AV839096	C 182	23.4	0.5	96	9	A1336671	A1336671 g9w2e01.x
C 110	24.2	0.5	90	14	D34482	D34482 CSR-179A8	C 183	23.4	0.5	97	14	BQ793717	BQ793717 AU007819
C 111	24.2	0.5	93	13	BM157203	BM157203 tV45d12.y	C 184	23.4	0.5	97	17	AZ402848	AZ402848 EST 2655
C 112	24.2	0.5	96	9	AU267203	AU267203 AU267203	C 185	23.4	0.5	99	9	A1452857	A1452857 t126e03.x
C 113	24.2	0.5	94	17	AZ822902	AZ822902 2M0096K06	C 186	23.4	0.5	100	9	AA809558	AA809558 nj43d12.s
C 114	24.2	0.5	97	14	BQ455711	BQ455711 ke21h06.y	C 187	23.4	0.5	100	12	BF748792	BF748792 MR0-BN011
C 115	24.2	0.5	98	17	BH847422	BH847422 SALK_0531	C 188	23.4	0.5	100	12	BF751061	BF751061 CM3-BN038
C 116	24.2	0.5	99	13	BQ644934	BQ644934 BU064494	C 189	23.4	0.5	100	14	BQ979553	BQ979553 OH185180
C 117	24.2	0.5	100	12	BF633479	BF633479 NF053B07D	C 190	23.4	0.5	62	9	AL655180	AL655180 AL655180
C 118	24.2	0.5	51	17	B03367	B03367 CSR-177B6	C 191	23.2	0.5	62	17	AZ481769	AZ481769 1M0306G13
C 119	23.8	0.5	64	10	AM626467	AM626467 SMOVAFARP	C 192	23.2	0.5	69	17	AZ576681	AZ576681 AST-TD1.4
C 120	23.8	0.5	64	10	AM626467	AM626467 SMOVAFARP	C 193	23.2	0.5	71	10	AA413615	AA413615 vcs7g04.s
C 121	23.8	0.5	72	17	AZ861143	AZ861143 SMOVAFARP	C 194	23.2	0.5	72	10	AM697232	AM697232 NF116E08S
C 122	23.8	0.5	72	17	AZ861143	AZ861143 SMOVAFARP	C 195	23.2	0.5	72	13	B1322719	B1322719 kx15d04.y
C 123	23.8	0.5	75	9	A1923606	A1923606 w175g12.x	C 196	23.2	0.5	72	13	B1322866	B1322866 kx09b07.y
C 124	23.8	0.5	84	14	BQ548336	BQ548336 rd24d09.y	C 197	23.2	0.5	74	13	B1322866	B1322866 kx13f05.y
C 125	23.8	0.5	87	9	AA553355	AA553355 ag65e01.s	C 198	23.2	0.5	75	13	B1322866	B1322866 kx12a10.y
C 126	23.8	0.5	87	9	AA553355	AA553355 ag65e01.s	C 199	23.2	0.5	74	13	B1322866	B1322866 kx12a10.y
C 127	23.8	0.5	88	14	BQ383621	BQ383621 NISC_mn02	C 200	23.2	0.5	80	13	B1742823	B1742823 OH185180
C 128	23.8	0.5	90	14	T40328	T40328 yA32c06.r2	C 201	23.2	0.5	81	9	A1798074	A1798074 we84c11.x
C 129	23.8	0.5	92	9	AA178419	AA178419 mt52e12.r	C 202	23.2	0.5	82	9	AA013827	AA013827 m04g005.r
C 130	23.8	0.5	92	14	BQ793758	BQ793758 EST 2696	C 203	23.2	0.5	82	9	AA013827	AA013827 m04g005.r
C 131	23.8	0.5	93	9	AA184929	AA184929 EST 2696	C 204	23.2	0.5	83	9	AA013827	AA013827 m04g005.r
C 132	23.8	0.5	93	17	AZ440614	AZ440614 1M0231G15	C 205	23.2	0.5	84	13	B1451149	B1451149 kx11d01.y
C 133	23.8	0.5	97	9	A1383005	A1383005 tc21f12.x	C 206	23.2	0.5	84	13	B1742935	B1742935 kx36h01.y
C 134	23.8	0.5	99	10	AM600205	AM600205 SMLCAK11	C 207	23.2	0.5	85	13	B1742935	B1742935 kx39h10.y
C 135	23.8	0.5	100	17	AZ373796	AZ373796 1M0126G13	C 208	23.2	0.5	86	12	BB881724	BB881724 601489953
C 136	23.8	0.5	100	10	AV954067	AV954067 AV954067	C 209	23.2	0.5	86	12	BB881724	BB881724 601489953
C 137	23.6	0.5	59	14	C21189	C21189 HUMGS000220	C 210	23.2	0.5	87	13	BH847310	BH847310 SALK_0523
C 138	23.6	0.5	69	9	AA388738	AA388738 v022b03.r	C 211	23.2	0.5	88	13	BG930167	BG930167 f3-c9.f3
C 139	23.6	0.5	73	12	BG310639	BG310639 SMOV3MCAM	C 212	23.2	0.5	88	13	B1742965	B1742965 kx34h11.y
C 140	23.6	0.5	76	9	AU012112	AU012112 AU012112	C 213	23.2	0.5	88	13	B1742965	B1742965 kx34h11.y
C 141	23.6	0.5	76	9	AU012112	AU012112 AU012112	C 214	23.2	0.5	89	13	B1742965	B1742965 kx34h11.y
C 142	23.6	0.5	77	9	A1564415	A1564415 t974h04.x	C 215	23.2	0.5	90	9	AA910888	AA910888 kx39e05.y
C 143	23.6	0.5	81	14	BQ795850	BQ795850 HSPD1991.H	C 216	23.2	0.5	90	9	A1988876	A1988876 kx35b11.y
C 144	23.6	0.5	87	9	AA231948	AA231948 AS31SB03	C 217	23.2	0.5	90	10	AV537201	AV537201 AV537201
C 145	23.6	0.5	88	17	AL757787	AL757787 Arabidops	C 218	23.2	0.5	90	13	B1742774	B1742774 kx34h09.y
C 146	23.6	0.5	89	17	AZ303890	AZ303890 1M0003P10	C 219	23.2	0.5	91	9	AA065877	AA065877 m152c09.r
C 147	23.6	0.5	89	17	AZ303890	AZ303890 1M0003P10	C 220	23.2	0.5	92	9	AA065877	AA065877 m152c09.r
C 148	23.6	0.5	89	17	AZ303890	AZ303890 1M0003P10	C 221	23.2	0.5	93	12	BF322806	BF322806 maa33h11.
C 149	23.6	0.5	91	17	AZ322634	AZ322634 1M0043P04	C 222	23.2	0.5	93	17	BH223849	BH223849 1006115D0
C 150	23.6	0.5	93	9	AA488835	AA488835 aa34h10.r	C 223	23.2	0.5	94	9	A1664252	A1664252 ue60e12.r
C 151	23.6	0.5	93	17	BH846992	BH846992 SALK_0125	C 224	23.2	0.5	94	9	A1664252	A1664252 ue60e12.r
C 152	23.6	0.5	94	17	CNS0201M	AL209335 Telradon	C 225	23.2	0.5	95	14	BQ393535	BQ393535 NISC_m904

226	23.2	0.5	95	14	H98130	H98130 yx10d06.sl	299	22.8	0.5	88	9	A1252396	A1252396 qv28h10.x
227	23.2	0.5	95	17	A2623818	A2623818 1M0461H19	300	22.8	0.5	89	10	BE316823	BE316823 NF066502L
228	23.2	0.5	96	17	A2950979	A2950979 2M0215P16	301	22.8	0.5	89	12	BF638868	BF638868 NF060104P
229	23.2	0.5	98	10	AM551886	AM551886 1O205B03-	302	22.8	0.5	90	1	A1988276	A1988276 SC98412.y
230	23.2	0.5	98	13	BM343075	BM343075 fW51C06.y	303	22.8	0.5	90	14	BO754116	BO754116 EB6301-SQ
231	23.2	0.5	99	10	AM852688	AM852688 AV852688	304	22.8	0.5	90	17	AL752638	AL752638 A161d0ps
232	23.2	0.5	99	10	BE166843	BE166843 CM2-HT050	305	22.8	0.5	91	14	AA663819	AA663819 aer7f01.s
233	23.2	0.5	99	14	T50985	T50985 yb71d01..s1	306	22.8	0.5	91	14	BQ255855	BQ255855 N1SC-1q06
234	23.2	0.5	99	17	TA242A060	TA242A060	307	22.8	0.5	92	10	AL679606	AL679606 AL679606
235	23.2	0.5	100	17	A1882508	A1882508 ubd7a08.1	308	22.8	0.5	92	10	AV531478	AV531478 AV531478
236	23.2	0.5	100	12	BE874679	BE874679 CM0-ET012	309	22.8	0.5	92	13	B1335801	B1335801 42-12.Hum
237	23.2	0.5	103	10	AV533029	AV533029 AVS33029	310	22.8	0.5	93	9	A1096771	A1096771 qa06h07.x
238	23.2	0.5	65	13	BJ049547	BJ049547 BJ049547	311	22.8	0.5	93	9	A1620635	A1620635 tu47h10.x
239	23.2	0.5	69	9	AA589335	AA589335 vm36905.t	312	22.8	0.5	94	9	AT004331	AT004331 AT004331
240	23.2	0.5	71	17	A2471347	A2471347 1M0285121	313	22.8	0.5	94	10	AV966686	AV966686 AV966686
241	23.2	0.5	72	17	A1638207	A1638207 ts97f107.x	314	22.8	0.5	94	10	AM189645	AM189645
242	23.2	0.5	77	13	BI962533	BI962533 1e51d07.y	315	22.8	0.5	98	9	A1340472	A1340472 ca86d11.x
243	23.2	0.5	80	17	CNS02YWM	AL198368 sdt0a03.y	316	22.8	0.5	98	17	AU270324	AU270324 AU270324
244	23.2	0.5	81	17	A2479949	AL216329 Telradon	317	22.8	0.5	98	17	AZ785762	AZ785762 1M0030A02
245	23.2	0.5	82	17	AA171633	AZ479949 1M0301J06	318	22.8	0.5	99	12	BG153740	BG153740 naq59c02.r1
246	23.2	0.5	82	17	AA171633	AA171633 z094a06.x	319	22.8	0.5	100	10	AV921214	AV921214 AV921214
247	23.2	0.5	83	10	AA504005	AA504005 nh39f05.s	320	22.8	0.5	100	12	BE658798	BE658798 CM1-1M004
248	23.2	0.5	83	10	AA504005	AA504005 xc71g06.x	321	22.8	0.5	100	14	BQ380842	BQ380842 k31e06.y
249	23.2	0.5	86	17	AZ404005	AZ404005 1M0172J01	322	22.8	0.5	100	14	CNS01XC7	CNS01XC7
250	23.2	0.5	86	17	AA442749	AA442749 zvg6a11.s	323	22.8	0.5	37	9	A1302081	A1302081 qv57e12.x
251	23.2	0.5	88	14	HI931	HI931 H.5apiens.D	324	22.8	0.5	56	10	AV519485	AV519485 AV519485
252	23.2	0.5	89	17	HSEXTK35	HSEXTK35	325	22.8	0.5	57	12	BG099228	BG099228 naq8d11.
253	23.2	0.5	90	13	BI364393	BI364393 qv37b04.x	326	22.8	0.5	57	12	AZ654880	AZ654880 1M0229M24
254	23.2	0.5	90	13	BI782005	BI782005 K104C03.y	327	22.8	0.5	59	10	AV519835	AV519835 AV519835
255	23.2	0.5	91	17	A2346732	A1366782 qv41d10.x	328	22.8	0.5	62	13	AZ477006	AZ477006 1M0296E17
256	23.2	0.5	92	17	A2346732	A2346732 1M0028B07	329	22.8	0.5	64	13	BI142468	BI142468 SMOV3KCM
257	23.2	0.5	93	13	BI7804741	BI7804741 lu42c05.x	330	22.8	0.5	67	12	BE383386	BE383386 602045048
258	23.2	0.5	93	13	BI7804741	BI7804741 lu42c05.x	331	22.8	0.5	69	13	BI219526	BI219526 602393603
259	23.2	0.5	93	13	BI7804741	BI7804741 lu42c05.x	332	22.8	0.5	71	9	BI779137	BI779137 EBrc01-SQ
260	23.2	0.5	94	9	AI088953	AI088953 yf66c04.s1	333	22.8	0.5	71	9	AA66198	AA66198 nc67b04.x
261	23.2	0.5	94	9	AI088953	AI088953 ou86b05.s	334	22.8	0.5	72	14	BM706635	BM706635 UI-E-COD
262	23.2	0.5	94	9	AI088953	AI088953 as40d02.x	335	22.8	0.5	75	9	AA689902	AA689902 v62h12.r
263	23.2	0.5	94	9	AI088953	AI088953 as40d02.x	336	22.8	0.5	75	9	AA689902	AA689902 v62h12.r
264	23.2	0.5	96	10	AM191884	AM191884 x176f08.x	337	22.8	0.5	76	17	AZ968712	AZ968712 2M0241K10
265	23.2	0.5	96	10	AM191884	AM191884 x176f08.x	338	22.8	0.5	77	17	BH864548	BH864548 SALK.0962
266	23.2	0.5	96	17	B32145	BQ235155 hds4f04.g	339	22.8	0.5	79	9	AI480073	AI480073 tm71h05.x
267	23.2	0.5	97	9	AL803618	AL803618	340	22.8	0.5	79	9	AI480073	AI480073 tm71h05.x
268	23.2	0.5	97	9	AL803618	AL803618	341	22.8	0.5	79	9	AI480073	AI480073 tm71h05.x
269	23.2	0.5	97	10	BE52631	BE52631 UI-M-A01-	342	22.8	0.5	79	10	AI659061	AI659061
270	23.2	0.5	97	14	BO127273	BO127273 1157h11.y	343	22.8	0.5	80	9	AI250495	AI250495
271	23.2	0.5	97	14	BO127273	BO127273 1157h11.y	344	22.8	0.5	80	9	AI250495	AI250495
272	23.2	0.5	98	10	AM516362	AM516362 fb36c04.y	345	22.8	0.5	81	17	AI311066	AI311066
273	23.2	0.5	98	10	AM516362	AM516362 fb36c04.y	346	22.8	0.5	81	17	AI311066	AI311066
274	23.2	0.5	99	13	BI557493	BI557493 60338225	347	22.8	0.5	82	9	AI572914	AI572914
275	23.2	0.5	99	13	BI557493	BI557493 60338225	348	22.8	0.5	82	9	AI572914	AI572914
276	23.2	0.5	100	9	AA474393	AA474393 sb31c05.y	349	22.8	0.5	82	10	BE282088	BE282088
277	23.2	0.5	100	9	AA474393	AA474393 sb31c05.y	350	22.8	0.5	84	9	AA180875	AA180875
278	23.2	0.5	100	9	AA590458	AA590458 vm24c05.t	351	22.8	0.5	85	9	AI685692	AI685692
279	23.2	0.5	100	13	BI033614	BI033614 PM1-N120	352	22.8	0.5	85	14	T61535	T61535
280	22.8	0.5	54	9	AI564489	AI564489 tq37h12.x	353	22.8	0.5	86	9	AI470691	AI470691
281	22.8	0.5	67	14	NA1028	NA1028 yv53c05.s1	354	22.8	0.5	86	9	AU009981	AU009981
282	22.8	0.5	68	17	AZ474039	AZ474039 1M0290E16	355	22.8	0.5	86	10	AV534836	AV534836
283	22.8	0.5	69	10	AM698388	AM698388 G234.g1an	356	22.8	0.5	86	10	AV519786	AV519786
284	22.8	0.5	69	17	AL760933	AL760933 Arabidops	357	22.8	0.5	87	10	AV532625	AV532625
285	22.8	0.5	69	17	CNS02YWM	AL216849 Tetradon	358	22.8	0.5	87	17	AL761571	AL761571
286	22.8	0.5	70	17	AZ796084	AZ796084 2M0051G04	359	22.8	0.5	88	10	AV563877	AV563877
287	22.8	0.5	71	13	BI736720	BI736720 603360410	360	22.8	0.5	89	9	AU007252	AU007252
288	22.8	0.5	76	17	AA260720	AA260720 va12h09.r	361	22.8	0.5	89	14	H0090826	H0090826
289	22.8	0.5	76	17	AA260720	AA260720 va12h09.r	362	22.8	0.5	91	9	AA014022	AA014022
290	22.8	0.5	77	14	F32860	AL763306 Arabidops	363	22.8	0.5	91	10	AV519886	AV519886
291	22.8	0.5	79	12	BF031392	F32860 HSPD25935.H	364	22.8	0.5	91	10	AV760647	AV760647
292	22.8	0.5	82	9	A1510767	A1510767 qv32f102.x	365	22.8	0.5	92	10	AI260047	AI260047
293	22.8	0.5	82	9	A1510767	BF031392 601559175	366	22.8	0.5	92	10	AM692461	AM692461
294	22.8	0.5	85	9	AA804737	AA804737 of48a08.s	367	22.8	0.5	92	14	R72581	R72581
295	22.8	0.5	85	9	AA935761	AA935761 on13f11.s	368	22.8	0.5	94	9	AI433403	AI433403
296	22.8	0.5	85	9	AA404572	AA404572 z141b03.r	369	22.8	0.5	94	9	AA487086	AA487086
297	22.8	0.5	86	17	BH227411	BH227411 1006139H0	370	22.8	0.5	94	14	R26640	R26640
298	22.8	0.5	87	9	AI251224	AI251224 qv39912.x	371	22.8	0.5	95	10	AV519671	AV519671

C 372	22.6	0.5	95	17	A2659464	A2659464	1M0536A22	445	22.4	0.4	100	12	BF087192
C 373	22.6	0.5	96	14	AA212521	AA212521	mw77b06.r	C 446	22.4	0.4	100	13	BJ435259
C 374	22.6	0.5	96	14	N21324	N21324	yx49a11.s1	447	22.4	0.4	100	14	BM733732
C 375	22.6	0.5	96	14	N27632	N27632	yw50c05.s1	448	22.2	0.4	45	9	AU258887
C 376	22.6	0.5	96	17	BM405867	BM405867	RPCI-23-8	449	22.2	0.4	53	17	BM609802
C 377	22.6	0.5	97	12	BF148426	BF148426	uy80h09.x	C 450	22.2	0.4	59	9	AA414885
C 378	22.6	0.5	98	13	BI193808	BI193808	qes5904.x	C 451	22.2	0.4	64	9	AA414885
C 379	22.6	0.5	98	13	BI259645	BI259645	602968541	C 452	22.2	0.4	64	9	AA414885
C 380	22.6	0.5	98	17	A2769905	A2769905	1M0571H05	C 453	22.2	0.4	64	9	AA414885
C 381	22.6	0.5	99	14	H38793	H38793	ym83q06.r1	C 454	22.2	0.4	64	12	BF400538
C 382	22.6	0.5	100	12	BF815228	BF815228	MR2-C1012	C 455	22.2	0.4	65	9	AU269389
C 383	22.6	0.5	100	13	BF086313	BF086313	BJ086313	C 456	22.2	0.4	69	13	BI676701
C 384	22.6	0.5	100	13	BF086313	BF086313	BJ086313	C 457	22.2	0.4	70	17	A2694534
C 385	22.4	0.4	58	17	B00351	B00351	CSR-108a2-	C 458	22.2	0.4	70	17	CNS0283X
C 386	22.4	0.4	58	17	A2499503	A2499503	1M0337M13	C 459	22.2	0.4	72	12	BM673201
C 387	22.4	0.4	63	14	BQ243213	BQ243213	TaE15017G	C 460	22.2	0.4	74	10	AV832572
C 388	22.4	0.4	67	9	AI538304	AI538304	lp6h10.x	C 461	22.2	0.4	74	17	A2490565
C 389	22.4	0.4	70	10	BF681222	BF681222	dq08a05.y	C 462	22.2	0.4	75	14	BM810491
C 390	22.4	0.4	72	9	AA500503	AA500503	v181g05.r	C 463	22.2	0.4	75	14	AA903811
C 391	22.4	0.4	73	9	AI61934	AI61934	ld18a10.x	C 464	22.2	0.4	75	14	BM523783
C 392	22.4	0.4	74	14	BQ795066	BQ795066	EST 4004	C 465	22.2	0.4	76	9	AI335738
C 393	22.4	0.4	74	14	BQ795066	BQ795066	EST 4427	C 466	22.2	0.4	78	14	C02363
C 394	22.4	0.4	76	14	BM541350	BM541350	ps63q07.y	C 467	22.2	0.4	78	17	A2381260
C 395	22.4	0.4	76	17	DR10N4S	DR10N4S	ret	C 468	22.2	0.4	79	9	AI537245
C 396	22.4	0.4	77	14	BQ795490	BQ795490	EST 4428	C 469	22.2	0.4	79	14	BQ266862
C 397	22.4	0.4	77	17	BM851619	BM851619	SALK_0732	C 470	22.2	0.4	80	14	AV851139
C 398	22.4	0.4	78	17	BM851619	BM851619	SALK_0990	C 471	22.2	0.4	80	14	F34720
C 399	22.4	0.4	79	17	BQ793571	BQ793571	EST 2509	C 472	22.2	0.4	81	9	AU007999
C 400	22.4	0.4	79	17	BM405787	BM405787	RPCI-23-2	C 473	22.2	0.4	81	10	AM323780
C 401	22.4	0.4	81	10	AA953855	AA953855	AY953855	C 474	22.2	0.4	82	14	F33148
C 402	22.4	0.4	83	9	AI505128	AI505128	vq69g02.x	C 475	22.2	0.4	83	9	AA671672
C 403	22.4	0.4	83	9	AI505128	AI505128	vq69g02.x	C 476	22.2	0.4	83	9	AA671672
C 404	22.4	0.4	83	12	BM058145	BM058145	nah21c04.y	C 477	22.2	0.4	83	9	AI6532703
C 405	22.4	0.4	84	14	BM733743	BM733743	k125d03.y	C 478	22.2	0.4	84	12	BG203583
C 406	22.4	0.4	84	14	BM733743	BM733743	k125d03.y	C 479	22.2	0.4	85	17	BG203583
C 407	22.4	0.4	85	10	AU257147	AU257147	sm22g05.y	C 480	22.2	0.4	86	12	BG234263
C 408	22.4	0.4	87	9	AA027165	AA027165	z693e12.s	C 481	22.2	0.4	86	12	BG234263
C 409	22.4	0.4	88	9	AI384188	AI384188	ld17f108.y	C 482	22.2	0.4	86	14	W52402
C 410	22.4	0.4	88	13	BM397269	BM397269	5009-0-30	C 483	22.2	0.4	86	14	W52402
C 411	22.4	0.4	88	13	BM397269	BM397269	EST 4168	C 484	22.2	0.4	87	17	BM800773
C 412	22.4	0.4	88	14	BM795230	BM795230	EST 4168	C 485	22.2	0.4	87	17	BM800773
C 413	22.4	0.4	89	17	A2587910	A2587910	1M0395119	C 486	22.2	0.4	87	17	AF038532
C 414	22.4	0.4	90	9	AI250604	AI250604	sc06b10.y	C 487	22.2	0.4	88	17	A2628049
C 415	22.4	0.4	91	9	AA952854	AA952854	SMRCEA00	C 488	22.2	0.4	89	9	AI918394
C 416	22.4	0.4	91	9	AI988660	AI988660	sc06b10.y	C 489	22.2	0.4	89	10	AM026944
C 417	22.4	0.4	91	14	N85628	N85628	J421IF Huma	C 490	22.2	0.4	90	13	BI493480
C 418	22.4	0.4	91	17	AL760481	AL760481	ArabiDops	C 491	22.2	0.4	91	17	A2343591
C 419	22.4	0.4	92	9	AI784233	AI784233	tw58b01.x	C 492	22.2	0.4	91	17	A2343591
C 420	22.4	0.4	93	9	AA502077	AA502077	pg72b07.s	C 493	22.2	0.4	92	13	BI257458
C 421	22.4	0.4	94	9	AI987884	AI987884	um08c10.x	C 494	22.2	0.4	92	13	BI257458
C 422	22.4	0.4	94	9	AA205202	AA205202	zq71n06.s	C 495	22.2	0.4	92	17	A2620200
C 423	22.4	0.4	94	9	AA215618	AA215618	zr795e06.r	C 496	22.2	0.4	93	9	AI331231
C 424	22.4	0.4	95	9	AA279608	AA279608	z888b02.r	C 497	22.2	0.4	93	9	AI331231
C 425	22.4	0.4	95	14	BQ793588	BQ793588	EST 2526	C 498	22.2	0.4	93	17	A2626144
C 426	22.4	0.4	95	14	W11427	W11427	ma90b07.r1	C 499	22.2	0.4	94	9	AI330911
C 427	22.4	0.4	95	17	A2779171	A2779171	2M0015M12	C 500	22.2	0.4	94	9	AI330911
C 428	22.4	0.4	96	9	AA823928	AA823928	vq93e05.r	C 501	22.2	0.4	94	14	N33799
C 429	22.4	0.4	96	9	AJ500170	AJ500170	AJ500170	C 502	22.2	0.4	95	9	AA174188
C 430	22.4	0.4	96	13	BJ031535	BJ031535	AJ5067171	C 503	22.2	0.4	95	14	N86930
C 431	22.4	0.4	97	13	BI979207	BI979207	hfe0676.s	C 504	22.2	0.4	95	17	CNS0321G
C 432	22.4	0.4	97	13	BI979207	BI979207	hfe0676.s	C 505	22.2	0.4	96	9	AI442889
C 433	22.4	0.4	97	13	BI979207	BI979207	hfe0676.s	C 506	22.2	0.4	96	14	E32461
C 434	22.4	0.4	97	14	BQ473504	BQ473504	AU267030	C 507	22.2	0.4	96	14	E32461
C 435	22.4	0.4	98	9	AA956469	AA956469	AV956469	C 508	22.2	0.4	96	14	W67634
C 436	22.4	0.4	98	10	AA956469	AA956469	AV956469	C 509	22.2	0.4	97	9	AA666986
C 437	22.4	0.4	98	14	H13520	H13520	y115b09.s1	C 510	22.2	0.4	97	9	AI080418
C 438	22.4	0.4	98	17	BM814666	BM814666	SALK_0667	C 511	22.2	0.4	97	9	AL820194
C 439	22.4	0.4	99	10	AM302439	AM302439	xr46h09.x	C 512	22.2	0.4	97	13	BM096718
C 440	22.4	0.4	99	12	BM894372	BM894372	rk51h04.y	C 513	22.2	0.4	97	17	AL754186
C 441	22.4	0.4	99	17	A2802736	A2802736	rm0061D16	C 514	22.2	0.4	98	10	AA459323
C 442	22.4	0.4	100	9	AA127365	AA127365	zn91h09.r	C 515	22.2	0.4	98	10	AA459323
C 443	22.4	0.4	100	10	AM065297	AM065297	614045E02	C 516	22.2	0.4	99	14	BM36233
C 444	22.4	0.4	100	12	BF680992	BF680992	602156276	C 517	22.2	0.4	99	17	BM36233

C 518	22.2	0.4	99	17	BH615045	BH615045 KG00582-.5	591	22	0.4	100	13	B1942718	B1942718 SK79A03.Y
C 519	22.2	0.4	100	9	AI617512	AI617512 zehnl705.	C 592	22	0.4	100	13	B1024186	B1024186 B1024186
C 520	22.2	0.4	100	9	AI988516	AI988516 s03d03.Y	C 593	22	0.4	100	13	B1342532	B1342532 B1342532
C 521	22.2	0.4	100	9	AI719053	AI719053 AIU79053	C 594	22	0.4	100	13	B1342532	B1342532 B1342532
C 522	22.2	0.4	100	9	AA629357	AA629357 V135908.r	C 595	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 523	22.2	0.4	100	9	AA624889	AA624889 vnr3908.r	C 596	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 524	22.2	0.4	100	12	BG258990	BG258990 602379012	C 597	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 525	22.2	0.4	100	12	BF095011	BF095011 PM1-UT006	C 598	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 526	22.2	0.4	100	13	BI001519	BI001519 MR3-HN014	C 599	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 527	22.2	0.4	100	17	AL768524	AL768524 AL768524	C 600	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 528	22.2	0.4	55	17	AA085966	AA085966 z183H12.S	C 601	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 529	22.2	0.4	64	17	AA085966	AA085966 z183H12.S	C 602	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 530	22.2	0.4	72	14	BH756304	BH756304 SALK-0534	C 603	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 531	22.2	0.4	69	17	BH756304	BH756304 SALK-0534	C 604	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 532	22.2	0.4	73	10	AI739189	AI739189 w127C11.X	C 605	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 533	22.2	0.4	73	10	AI739189	AI739189 w127C11.X	C 606	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 534	22.2	0.4	73	10	AI739189	AI739189 w127C11.X	C 607	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 535	22.2	0.4	73	10	AI739189	AI739189 w127C11.X	C 608	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 536	22.2	0.4	74	17	BH857828	BH857828 SALK-0874	C 609	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 537	22.2	0.4	74	17	BH857828	BH857828 SALK-0874	C 610	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 538	22.2	0.4	75	10	AA615120	AA615120 vnr02b09.r	C 611	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 539	22.2	0.4	75	10	AA615120	AA615120 vnr02b09.r	C 612	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 540	22.2	0.4	77	10	BE320162	BE320162 NF025H03R	C 613	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 541	22.2	0.4	77	12	BE320162	BE320162 NF025H03R	C 614	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 542	22.2	0.4	77	12	BE320162	BE320162 NF025H03R	C 615	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 543	22.2	0.4	77	14	BO456810	BO456810 KE31C12.Y	C 616	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 544	22.2	0.4	77	14	BO456810	BO456810 KE31C12.Y	C 617	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 545	22.2	0.4	77	14	BO456810	BO456810 KE31C12.Y	C 618	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 546	22.2	0.4	78	10	AV949979	AV949979 AV949979	C 619	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 547	22.2	0.4	79	17	AV844464	AV844464 AV844464	C 620	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 548	22.2	0.4	79	17	AV844464	AV844464 AV844464	C 621	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 549	22.2	0.4	80	9	AI469588	AI469588 tml407.X	C 622	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 550	22.2	0.4	80	17	AI469588	AI469588 tml407.X	C 623	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 551	22.2	0.4	80	17	AI469588	AI469588 tml407.X	C 624	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 552	22.2	0.4	82	9	AI764243	AI764243 tml407.X	C 625	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 553	22.2	0.4	82	9	AI764243	AI764243 tml407.X	C 626	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 554	22.2	0.4	83	14	BO391586	BO391586 NTSC-mq11	C 627	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 555	22.2	0.4	84	17	BO391586	BO391586 NTSC-mq11	C 628	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 556	22.2	0.4	85	17	AA107738	AA107738 mc48e04.r	C 629	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 557	22.2	0.4	86	17	AA506305	AA506305 nh45a08.S	C 630	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 558	22.2	0.4	87	17	AA506305	AA506305 nh45a08.S	C 631	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 559	22.2	0.4	88	17	BH857820	BH857820 SALK-0874	C 632	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 560	22.2	0.4	88	17	BH857820	BH857820 SALK-0874	C 633	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 561	22.2	0.4	88	12	BG152617	BG152617 na157h09.	C 634	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 562	22.2	0.4	88	13	BM027242	BM027242 GIT000056	C 635	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 563	22.2	0.4	88	13	BM027242	BM027242 GIT000056	C 636	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 564	22.2	0.4	88	13	BM027242	BM027242 GIT000056	C 637	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 565	22.2	0.4	91	9	AI933472	AI933472 wnr4a04.X	C 638	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 566	22.2	0.4	92	17	BH857820	BH857820 SALK-0874	C 639	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 567	22.2	0.4	92	17	BH857820	BH857820 SALK-0874	C 640	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 568	22.2	0.4	93	17	AI828270	AI828270 na157h09.	C 641	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 569	22.2	0.4	93	17	AI828270	AI828270 na157h09.	C 642	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 570	22.2	0.4	94	12	BG391993	BG391993 602409941	C 643	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 571	22.2	0.4	94	12	BG391993	BG391993 602409941	C 644	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 572	22.2	0.4	95	9	AI014994	AI014994 602409941	C 645	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 573	22.2	0.4	96	13	BI499032	BI499032 1e28g09.X	C 646	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 574	22.2	0.4	97	9	AA714476	AA714476 na157h09.	C 647	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 575	22.2	0.4	97	9	AA714476	AA714476 na157h09.	C 648	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 576	22.2	0.4	97	9	AA714476	AA714476 na157h09.	C 649	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 577	22.2	0.4	97	12	BG057467	BG057467 r135c02.Y	C 650	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 578	22.2	0.4	98	10	AA190110	AA190110 mtr1e08.r	C 651	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 579	22.2	0.4	98	10	AA190110	AA190110 mtr1e08.r	C 652	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 580	22.2	0.4	98	12	BF651089	BF651089 NF101A01E	C 653	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 581	22.2	0.4	98	14	BF651089	BF651089 NF101A01E	C 654	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 582	22.2	0.4	98	14	BF651089	BF651089 NF101A01E	C 655	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 583	22.2	0.4	99	9	AI988193	AI988193 SC96d07.Y	C 656	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 584	22.2	0.4	99	9	AI988193	AI988193 SC96d07.Y	C 657	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 585	22.2	0.4	99	9	AI988193	AI988193 SC96d07.Y	C 658	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 586	22.2	0.4	100	9	AA013890	AA013890 mh07h11.r	C 659	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 587	22.2	0.4	100	9	AA013890	AA013890 mh07h11.r	C 660	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 588	22.2	0.4	100	9	AA013890	AA013890 mh07h11.r	C 661	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 589	22.2	0.4	100	9	AA013890	AA013890 mh07h11.r	C 662	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S
C 590	22.2	0.4	100	13	BI024076	BI024076 CM3-MT035	C 663	21.8	0.4	100	13	AA661435	AA661435 AK15H10.S

C 664	21.8	0.4	93	9	AU013433	AU013433	C 737	21.6	0.4	82	13	B3055136	B3055136
C 665	21.8	0.4	93	13	BM455282	BM455282 EBem09-SQ	C 738	21.6	0.4	83	9	AA680618	AA680618
C 666	21.8	0.4	93	14	BM879727	BM879727 KL9B09.Y	C 739	21.6	0.4	83	9	AA814174	AA814174
C 667	21.8	0.4	93	14	BQ334543	BQ334543 h446f11.g	C 740	21.6	0.4	83	10	AA639304	AA639304
C 668	21.8	0.4	93	14	BQ386012	BQ386012 NISC.mn15	C 741	21.6	0.4	84	9	AA591819	AA591819
C 669	21.8	0.4	93	14	BQ788232	BQ788232 hw63d04.g	C 742	21.6	0.4	84	13	BA137764	BA137764
C 670	21.8	0.4	93	17	AZ305460	AZ305460 1M0006H11	C 743	21.6	0.4	85	9	AA637555	AA637555
C 671	21.8	0.4	93	17	BH128522	BH128522 G-3h15.r	C 744	21.6	0.4	85	9	AU265253	AU265253
C 672	21.8	0.4	94	9	AL836084	AL836084 0155604.s	C 745	21.6	0.4	85	14	BM955050	BM955050
C 673	21.8	0.4	94	10	AN140194	AN140194 SWAMC44	C 746	21.6	0.4	86	17	AZ380924	AZ380924
C 674	21.8	0.4	94	12	BE908034	BE908034 601500242	C 747	21.6	0.4	86	12	BE881724	BE881724
C 675	21.8	0.4	94	14	BQ788464	BQ788464 hw67b12.9	C 748	21.6	0.4	87	14	N34848	N34848
C 676	21.8	0.4	94	17	AZ479471	AZ479471 1M0300B07	C 749	21.6	0.4	87	17	AZ780952	AZ780952
C 677	21.8	0.4	95	14	W89778	W89778 mf75c11.r1	C 750	21.6	0.4	88	9	AA068421	AA068421
C 678	21.8	0.4	95	17	AZ576188	AZ576188 AST-TD12-	C 751	21.6	0.4	88	9	AU046593	AU046593
C 679	21.8	0.4	95	17	AL763855	AL763855 Arabidops	C 752	21.6	0.4	88	10	BE325908	BE325908
C 680	21.8	0.4	95	17	CNS0608X	AL415543 t7 end of	C 753	21.6	0.4	88	17	AZ956706	AZ956706
C 681	21.8	0.4	96	9	AA766618	AA766618 0a33h12.s	C 754	21.6	0.4	89	9	AA403229	AA403229
C 682	21.8	0.4	96	9	AT883268	AT883268 1096b10.x	C 755	21.6	0.4	89	9	AA483286	AA483286
C 683	21.8	0.4	96	9	AT883268	AZ427959 1M0210C16	C 756	21.6	0.4	89	12	BG910719	BG910719
C 684	21.8	0.4	96	9	AT883268	AZ427959 1M0210C16	C 757	21.6	0.4	89	17	AL756224	AL756224
C 685	21.8	0.4	96	17	AZ427959	AZ427959 sp43h09.Y	C 758	21.6	0.4	89	17	AL756224	AL756224
C 686	21.8	0.4	97	9	AI930887	AI930887 zp43h09.Y	C 759	21.6	0.4	89	17	AL756224	AL756224
C 687	21.8	0.4	97	9	AA179461	AA179461 zp43h09.Y	C 760	21.6	0.4	89	17	AL756224	AL756224
C 688	21.8	0.4	97	10	AA678563	AA678563 AV678563	C 761	21.6	0.4	90	2	HSM003105	HSM003105
C 689	21.8	0.4	97	10	AA678563	AA678563 0a26f05.x	C 762	21.6	0.4	90	12	BG153212	BG153212
C 690	21.8	0.4	97	14	CA84172	CA84172 CA8172 Dict	C 763	21.6	0.4	91	9	AA939615	AA939615
C 691	21.8	0.4	97	17	BH849830	BH849830 SALK_0703	C 764	21.6	0.4	91	14	BQ126492	BQ126492
C 692	21.8	0.4	98	9	AL500931	AL500931 AJ500931	C 765	21.6	0.4	91	12	BG562086	BG562086
C 693	21.8	0.4	98	13	BI493234	BI493234 AJ500931	C 766	21.6	0.4	91	13	BF109271	BF109271
C 694	21.8	0.4	98	13	BJ047711	BJ047711 BJ047711	C 767	21.6	0.4	91	13	BM068861	BM068861
C 695	21.8	0.4	98	17	BH848162	BH848162 SALK_0675	C 768	21.6	0.4	92	17	AZ824717	AZ824717
C 696	21.8	0.4	99	9	AJ500079	AJ500079 AJ500079	C 769	21.6	0.4	92	17	BH413191	BH413191
C 697	21.8	0.4	99	17	BH863371	BH863371 SALK_0937	C 770	21.6	0.4	92	17	BH847962	BH847962
C 698	21.8	0.4	100	9	AA683899	AA683899 v06f01.r	C 771	21.6	0.4	93	10	AL797662	AL797662
C 699	21.8	0.4	100	9	AA683899	AA683899 am23d07.s	C 772	21.6	0.4	93	9	AO909097	AO909097
C 700	21.8	0.4	100	9	AI767200	AI767200 w194c05.x	C 773	21.6	0.4	93	14	BQ235010	BQ235010
C 701	21.8	0.4	100	10	AA336968	AA336968 77621 MAR	C 774	21.6	0.4	93	17	AZ848413	AZ848413
C 702	21.8	0.4	100	10	AA336968	AA336968 77621 MAR	C 775	21.6	0.4	94	9	AA727090	AA727090
C 703	21.8	0.4	100	12	BE906284	BE906284 601502275	C 776	21.6	0.4	94	9	AA1201345	AA1201345
C 704	21.8	0.4	100	13	BI491202	BI491202 dT05d01.w	C 777	21.6	0.4	94	9	AA106067	AA106067
C 705	21.8	0.4	100	13	BM090987	BM090987 1q18h03.x	C 778	21.6	0.4	94	9	AA165347	AA165347
C 706	21.8	0.4	100	13	BM090987	BM090987 1q18h03.x	C 779	21.6	0.4	94	9	AA165347	AA165347
C 707	21.8	0.4	100	13	BM090987	BM090987 1q18h03.x	C 780	21.6	0.4	94	9	AA165347	AA165347
C 708	21.8	0.4	100	14	N22603	N22603 yw31e03.s1	C 781	21.6	0.4	95	12	BF225188	BF225188
C 709	21.8	0.4	100	14	N22603	N22603 yw31e03.s1	C 782	21.6	0.4	95	14	WA7155	WA7155
C 710	21.8	0.4	100	17	TH339604Q	TH339604Q T. brucei	C 783	21.6	0.4	95	17	AZ576154	AZ576154
C 711	21.6	0.4	55	9	AA832657	AA832657 vW45a01.r	C 784	21.6	0.4	96	9	AU008340	AU008340
C 712	21.6	0.4	55	12	BG153530	BG153530 naq49h05.	C 785	21.6	0.4	96	9	AU008340	AU008340
C 713	21.6	0.4	55	12	BG153530	BG153530 naq49h05.	C 786	21.6	0.4	96	14	BQ636146	BQ636146
C 714	21.6	0.4	55	14	H14140	H14140 ym65f05.r1	C 787	21.6	0.4	96	17	AZ854992	AZ854992
C 715	21.6	0.4	57	17	B03689	B03689 GSR1-185A1-	C 788	21.6	0.4	97	9	A1036529	A1036529
C 716	21.6	0.4	58	9	AI473789	AI473789 tm03d02.x	C 789	21.6	0.4	97	9	A1255137	A1255137
C 717	21.6	0.4	58	17	AZ656081	AZ656081 1M0531j19	C 790	21.6	0.4	97	9	A1321720	A1321720
C 718	21.6	0.4	59	9	AI880479	AI880479 ac78d09.x	C 791	21.6	0.4	97	9	A1540563	A1540563
C 719	21.6	0.4	63	13	BI412820	BI412820 602989394	C 792	21.6	0.4	97	12	BF434734	BF434734
C 720	21.6	0.4	64	9	AA522905	AA522905 n141d05.s	C 793	21.6	0.4	97	17	AZ514087	AZ514087
C 721	21.6	0.4	66	9	AU265888	AU265888 0263888	C 794	21.6	0.4	97	17	CNS0251V	CNS0251V
C 722	21.6	0.4	67	9	AA191154	AA191154 zp86e08.r	C 795	21.6	0.4	97	17	CNS048V0	CNS048V0
C 723	21.6	0.4	68	9	AA1139634	AA1139634 qe02f06.x	C 796	21.6	0.4	98	12	BF593054	BF593054
C 724	21.6	0.4	70	9	AA922430	AA922430 0153f05.s	C 797	21.6	0.4	98	12	BG175207	BG175207
C 725	21.6	0.4	70	14	W58297	W58297 zd19a06.r1	C 798	21.6	0.4	98	14	BQ393450	BQ393450
C 726	21.6	0.4	71	9	AU256317	AU256317 AU256317	C 799	21.6	0.4	98	14	N51544	N51544
C 727	21.6	0.4	73	9	AA397711	AA397711 zt87f05.r	C 800	21.6	0.4	98	17	BE4073033	BE4073033
C 728	21.6	0.4	74	17	AZ851480	AZ851480 2M0153D13	C 801	21.6	0.4	99	10	BE4073033	BE4073033
C 729	21.6	0.4	75	10	AA696083	AA696083 NF101F10S	C 802	21.6	0.4	99	12	BG170557	BG170557
C 730	21.6	0.4	75	10	AA696083	AA696083 NF101F10S	C 803	21.6	0.4	99	12	BG170557	BG170557
C 731	21.6	0.4	77	10	AA696083	AA696083 NF101F10S	C 804	21.6	0.4	99	13	BI813983	BI813983
C 732	21.6	0.4	77	10	AA696083	AA696083 NF101F10S	C 805	21.6	0.4	99	14	BM935438	BM935438
C 733	21.6	0.4	77	10	AA696083	AA696083 NF101F10S	C 806	21.6	0.4	99	14	BM935438	BM935438
C 734	21.6	0.4	77	10	AA696083	AA696083 NF101F10S	C 807	21.6	0.4	99	17	AZ756344	AZ756344
C 735	21.6	0.4	79	10	AA696083	AA696083 NF101F10S	C 808	21.6	0.4	99	17	AZ756344	AZ756344
C 736	21.6	0.4	82	9	AA260536	AA260536 vD06d08.r	C 809	21.6	0.4	99	17	AL770229	AL770229





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This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:699731
Seq primer: -28mj rev2 EF from Amersham
High quality sequence stop: 82.
Location/Qualifiers
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organism="Mus musculus"
strain="C57BL/6J"
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clone.lib=Soares_thymus_2nbwt
sex="male"
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polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dt) primer [5']
TGTTACCAATCTGGAAGTCGGAGCGCCGCCTTTTTTTTTTTTTTTTTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Paloma Bonaldo."
BASE COUNT      27 a          26 g          23 t
ORIGIN
Query Match       0.8%; Score 39.8; DB 9; Length 95;
Best Local Similarity 70.7%; Pred.No.14;
Matches   53; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY  4471 GAATAACCCTAGTAGATTATGACTGTGAAATTCCTTAATCAGTCTGTATGTAATA 4530
     ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16  GAACGAGCCCCGTGCTAAGTAGTGCTGAGACAAGAATCCCCTGATCACATCTATATGTAATA 75
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY  4531 TTTCACATTAAGACTG 4545
     ||||||| |||||
Db  76  TTTCACATTAAGACTG 90

```

FEATURES	source
LOCUS	DR12A12S
DEFINITION	Danio rerio genomic clone Dkey-12A12, genomic survey sequence.
ACCESSION	AL743114
VERSION	AL743114.1
KEYWORDS	GI:21340560
SOURCE	GSS.
ORGANISM	zebrafish.
REFERENCE	Danio rerio.
AUTHORS	Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
JOURNAL	Cypriniformes; Cyprinidae; Danio.
COMMENT	1 (bases 1 to 64) Humphray,S.J., Huckle,E. and Hunt,S.E. Direct Submission Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphreysanger.ac.uk Unpublished This sequence was generated from the sp6 end of BAC 12A12. 12A12 is part of the Daniokey Pilot BAC Library created by R. Plasterk and N.V. Keygene. Further details: <a href="http://www.sanger.ac.uk/Projects/D-rerio/">http://www.sanger.ac.uk/Projects/D-rerio/</a> . Location/Qualifiers 1..64 /organism="Danio rerio" /db_xref="taxon:7955" /clone="Dkey-12A12"

```

/tissue_type="testis"
/note="vector pindigobac-536"
BASE COUNT      18 a      7 c      9 g      30 t
ORIGIN

Query Match
Best Local Similarity 67.7%; Pred. No. 5.8e+03;
Matches 42; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 4906 TCCAGCTTTGATGCAAGGCTGATTACGAAATTAGAAAGGTTCTTTTTCAA 4965
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3 TGTGTTTCTTCTGTAATAGTTCATGACACCGACCTAGTATTAAGATTCTTTTAA 62
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 4966 TA 4967
      ||
DB 63 TA 64

RESULT 3
AA490364      70 bp      mRNA      linear      EST 08-AUG-1997
LOCUS      aa490364.1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:823794 5'
DEFINITION      similar to SW:NM116098 P48479 PROTEIN KINASE NIM-1; mRNA
ACCESSION      AA490364
VERSION      AA490364.1 GI:2219537
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 70)
AUTHORS      Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Stepec, M., Tan, F., Theisling, B., White, Y., Wyllie,
J., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
JOURNAL      Unpublished (1997)
COMMENT      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 RT from Amersham
High quality sequence stop: 1.
FEATURES
Source
Location/Qualifiers
1..70
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:823794"
/clone_lib="Soares_NHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker. Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NHM, pregnant uterus
NHMPu, and fetal heart NHH19W) were mixed, and ss circles
were used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1 M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT      19 a      16 c      15 g      20 t
ORIGIN

Query Match
Best Local Similarity 71.7%; Pred. No. 1.1e+04;
Matches 38; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 4051 AATATCTTCTTCACCTCATCTGATTATCAACTGACAGATTGATGATTC 4103
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 8 AATATCTTCTTCACCTCATCTGATTATCAACTGACAGATTGATGATTC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
A1767078      71 bp      mRNA      linear      EST 21-DEC-1999
LOCUS      w192907.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:240828 3',
DEFINITION      mRNA sequence.
ACCESSION      A1767078
VERSION      A1767078.1 GI:5233587
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 71)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: c9gaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrrp/image/image.html
Insert length: 785 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 70.
FEATURES
Source
Location/Qualifiers
1..71
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:240828"
/clone_lib="NCI CGAP K1d12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker. Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_K1d5 was
prepared, and ss circles were used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1323912-1323831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Patina Bonaldo."
BASE COUNT      22 a      16 c      7 g      26 t
ORIGIN

Query Match
Best Local Similarity 64.2%; Pred. No. 1.5e+04;
Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 3085 TTGATTTTTCACAGCAATGCACTGCTTATTTACGCTTACCAAGATGACTTC 3144
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2 TTTTCTTGGCAGACACAGATTAATTAATTAACAATGACACGGAATGCTTC 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 3145 TTGATTT 3151
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 62 TTGATTT 68
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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```

/clone="IMAGE:2019185"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/label="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I oligo(dT) primer (5'
TGTTCACATCTGAAGTGGAGCGCCGACATAGGTTTATTTTATTTTATTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaudo."

BASE COUNT      19 a      6 c      4 g      54 t
ORIGIN
Query Match      0.6%; Score 27.8; DB 9; Length 83;
Best Local Similarity 59.5%; Pred. No. 2.6e+04;
Matches 47; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 475 TTTGAACTTACAGCTTGTAAAGCTTACCTGATCGTCAAGAGAGACAGAGAG 534
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 TTTAAATTTTAAATTTTCTTAAGTCAAGCTTGGGTTTAAAGAAAAA 24
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 535 CAAGAGACAGAGAAATA 553
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 AAAAAA 5

RESULT 8
BI322285 94 bp mRNA linear EST 30-JUL-2001
LOCUS kx19a08.y3 Parastromyloides trichosuri FL PAMPI v1 Chiapelli
DEFINITION McCarter Parastromyloides trichosuri cDNA 5', mRNA sequence.
ACCESSION BI322285.1 GI:15001471
VERSION EST
KEYWORDS Parastromyloides trichosuri.
SOURCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
ORGANISM Panagrolaimidae; Stromyloidae; Parastromyloides.
REFERENCE 1 (bases 1 to 94)
AUTHORS McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.,
Dante, M., Maitre, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y.,
Gibbons, M., Ritzer, E., Bennett, J., Franklin, C., Tsagaris, H., R.,
Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,
M., Allen, M., Person, B., Swalley, T., Harvey, N., Schurk, R., Kohne, S.,
Shin, T., Jackson, T., Cardenas, M., McCann, R., Waterston, R. and
Wilson, R.
JOURNAL The Washington Univ. Nematode EST Project, 1999
COMMENT Unpublished (1999)
CONTACT: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapelli@wustl.edu & jmcarter@wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
putative full length read
the vector to vector length is 95
Seq primer: -40RP from gibco.
FEATURES
Source 1. 94
/organism="Parastromyloides trichosuri"
/db_xref="taxon:131310"
/clone_lib="Parastromyloides trichosuri FL PAMPI v1
Chiapelli McCarter"
/dev_stage="free living"
/lab_host="DH10B"
/lab_note="DH10B"

/clone="IMAGE:2019185"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/label="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I oligo(dT) primer (5'
TGTTCACATCTGAAGTGGAGCGCCGACATAGGTTTATTTTATTTTATTTT
T 3'); double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaudo."

BASE COUNT      42 a      9 c      12 g      31 t
ORIGIN
Query Match      0.6%; Score 27.8; DB 13; Length 94;
Best Local Similarity 62.0%; Pred. No. 2.7e+04;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 3542 AGAAGTCAGTCCGATTTGTAAGAAAGAGTACCGGAATGAGAGAAAGATATCA 3601
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 AAAATTAGATCCAGTCAATGAAATTAAGACACATCAAAAAAGAGCTGTATATATTT 67
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3602 TTGGTCAAGTT 3612
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 TTTATCAAGTT 78

RESULT 9
AA154655/c
LOCUS AA154655
DEFINITION
ACCESSION AA154655.1 GI:1726483
VERSION EST
KEYWORDS Mus musculus.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Maitre, M., Hillier, L., Allen, M., Bowers, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
JOURNAL The WashU-HMMI Mouse EST Project
COMMENT Unpublished (1996)
CONTACT: Maitre M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:357862
Trace considered overall poor quality
possible reversed clone; similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
FEATURES
Source 1. 100
/organism="Mus musculus"
/strain="57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:363214"
/clone_lib="Soares_thymus_2NBMT"
/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/label="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

```

(Pharmacis), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pRR73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Patricia Bonaldo. "

Dy 944 CTGCAAAAGACTTCCAGACAGGGTGCGAGCAGCTGTGTTGGTTAAACATCACAAAAG 1003  
+ | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 86 CAAACAAGCGCGTNTAAGCCAGCGTCAGAGCANGCNGCTGGGTAAATMAAGANINCAACACAGN 27

QY	1004	ACTTAATCAGAAATTAG	1022
Db	26	ANAAATCAGAAAAAG	8

Db 26 ANAATACAGAAAGNAAAG

LOCUS	AI054386	98 bp	mRNA	linear	EST 27-JUL-1999
DEFINITION	q17e03.x1 NCI_CGAP_Ov26 Homo sapiens CDNA clone IMAGE:1862428 3', mRNA sequence.				

ORGANISM    Homo sapiens  
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
**JOURNAL** Unpublished (1997)

Issue Procurement: Monica Brown, M.D., Elise Kohn, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Analysis: David B. Krizman, Ph.D.

```

/lab_host="DH10B"
/notem="Oregon, summer, Western, August"

```

Query Match	0.58;	Score 27.4;	DB 9;	Length 98;
-------------	-------	-------------	-------	------------

QY 1127 AGGGTGTATCACACAGAGGAGATTTAAGGACTTGGAAAGTAGTACCGATGAGACTGAA 1186  
||||| ||| | | ||| ||||| ||||| | | ||| ||||| ||

Db	75	AGGGGAGAGAAATGCAAAAGAGATTAGAGGAGACAAAGATTAAGAGAGAGAAAAA	16
Qy	1187	AAGACAAA	1195
Db	15	AAAAAAAAA	7
RESULT 12			
LOCUS	AU254327/c	88 bp	mRNA
DEFINITION	AU254327 3'-directed mouse cDNA library Mus musculus cDNA clone		
VERSION	BE0001610	3', mRNA sequence.	
KEYWORDS	AU254327		
SOURCE	AU254327.1	GI:20316003	
ORGANISM	EST.		
REFERENCE	house mouse.		
AUTHORS	Mus musculus.		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
COMMENT	1 (bases 1 to 88)		
	Kato, K. and Matoba, R.		
	Generation of expressed sequence tags from mouse brain		
	Unpublished (2002)		
	Contact: Kikuya Kato		
	Graduate School of Biological Sciences		
	Nara Institute of Science and Technology		
	8916-5 Takayama, Ikoma, Nara 630-0101, Japan		
	Tel: 81-743-72-5581		
	Fax: 81-743-72-5589		
	Email: kkatoids.aist-nara.ac.jp,		
	URL: http://love2.aist-nara.ac.jp/BE0/ index.html.		
FEATURES	location/Qualifiers		
SOURCE	1..88		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
	/clone="BE0001610"		
	/clone_lib="3'-directed mouse cDNA library"		
	/listseq_type="brain"		
	/note="Vector: pGEM-T-easy"		
BASE COUNT	49 a 15 c 6 g 18 t		
ORIGIN			
Query Match	0.5%; Score 26.8; DB 9; Length 88;		
Best Local Similarity	57.0%; Pred. No. 4.9e+04;		
Matches 49; Conservative	0; Mismatches 37; Indels 0; Gaps 0		
Qy	4837	TTTTTAATCCTCGTTGTTGGTAGCATGCACTGTGAACCTTTTACCTTTTGTGTTG	4896
Db	88	TTTAAATGTTTGTGTTTAAAGCTGCGTGTTCACAAATTTATTTGTTGTGTTG	29
Qy	4897	TTGGCAAGCTCAGGTTTGATGCA	4922
Db	28	TTTTTATTGTGGTGCAATATATGGA	3
RESULT 13			
LOCUS	AL760836/c	90 bp	DNA
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-203807-014506,		
ACCESSION	AL760836		
VERSION	AL760836.1	GI:21500827	
KEYWORDS	GSS		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
	Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.		
	and Weissbach, B.		
	A pipeline for automated high-throughput generation of ESTs		
	(flanking sequence tags) from Arabidopsis thaliana T-DNA		

JOURNAL	transformed lines
REFERENCE	unpublished
AUTHORS	2
TITLE	Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
JOURNAL	A new Arabidopsis thaliana T-DNA mutagenised population. (GABI-Kat)
REFERENCE	for flanking sequence tag based reverse genetics
AUTHORS	unpublished
TITLE	3 (bases 1 to 90)
JOURNAL	Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
COMMENT	Direct Submission Submitted (17-JUN-2002) Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MN10. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <a href="http://www.mpiz-koeln.mpg.de/GABI-Kat/">http://www.mpiz-koeln.mpg.de/GABI-Kat/</a>
FEATURES	Location/Qualifiers 1..90 /organism="Arabidopsis thaliana" /strain="Columbia 0" /db_xref="taxon:3702" /clone="GK-203B07-014506" /clone_1fb="Arabidopsis thaliana T-DNA insertion lines" /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"
BASE COUNT	30 a 16 c 13 g 31 t
ORIGIN	
Query Match	0.5%: Score 26.8; DB 17; Length 90;
Best Local Similarity	64.5%: Pred. No. 5e+04; 22; Indels 0; Gaps 0;
Matches	40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY	4900 GCAAGCTGCAGGTTTGTAATGCAAAAGGCTGATATTCATTAATTAAGAAAGGCTCTT 4959
Db	77 GCAATCGAGAGTCATGTTATGCAATGACATGATCACTTATATGTTATGCAAAATCATTTGTTA 18
OY	4960 TT 4961
Db	17 TT 16
RESULT 14	
AV960997	98 bp mRNA linear EST 14-MAR-2002
LOCUS	AV960997
DEFINITION	AV960997 Nori Satoh unpublished cDNA library, cleavage stage embryo
ACCESSION	AV960997
VERSION	AV960997.1 GI:19449296
KEYWORDS	EST.
SOURCE	Ciona intestinalis.
ORGANISM	Ciona intestinalis Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; phlebobranchia; Clonidae; Ciona.
REFERENCE	1 (bases 1 to 98)
AUTHORS	Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.
TITLE	Expressed genes in Ciona intestinalis
JOURNAL	Unpublished. (2000)
COMMENT	Contact: Nori Satoh Department of Zoology Kyoto University Sakyo-Ku, Kyoto 606-8502, Japan Tel.: 81-75-753-4081 Fax: 81-75-705-1113







/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1588653"  
 /clone\_lib="NCI CGAP Kids"  
 /tissue\_type="2 pooled tumors (clear cell type)"  
 /lab\_host="DH10B"  
 /note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AACTGGAAGATTGCGCGCCGCAATATTTTATTAAGTCCCTAC 3') double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

## BASE COUNT

31 a 6 c 12 g 46 t

Query Match 0.5%; Score 26.4; DB 9; Length 95;  
 Best Local Similarity 59.2%; Pred. No. 6.5e+04;  
 Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 4876 CCTTACCTTTTGTGTTGTCAGTCGACGTTTGAATGCAAGCGTGATTAC 4935  
 ||||| ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 92 CTTTACTTTTGTATTGTAGTCTCAAGACCTTTTAAATAATTAAGTCCCTAC 33  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 4936 TGAATTTAAGAAAA 4951  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 32 TTACACTTAAAAAAA 17

## RESULT 20

R93104  
 LOCUS EST000038 S. mansoni cDNA Schistosoma mansoni cDNA clone  
 DEFINITION SMTBADAMS0038SK 5' end, mRNA sequence.  
 R93104  
 VERSION R93104.1 GI:965458  
 KEYWORDS EST.  
 SOURCE Schistosoma mansoni.  
 ORGANISM Schistosoma mansoni.  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.  
 1 (bases 1 to 95)  
 Sabar, M.A., Hamid, H., ElYassaki, W.M., Romeih, M., Ahmed, H., Mohareb  
 M., ElDabaa, I. and Mamdouh, S.  
 Schistosoma mansoni CDNS  
 Unpublished (1995)  
 Contact: M.A. Sabar, H. Hamid, W.M. El Yassaki, M. Romeih, H.  
 Ahmed, M. Mohareb, I. El Dabaa, S. Mamdouh  
 TBRI Biochemistry  
 Theodor Bilharz Research Institute  
 Imbaba, P.O.Box 12411, Giza, Egypt  
 Tel: 202 3128276  
 Fax: 202 3121167  
 Email: M-Sabar@FRCU.EUN.EG  
 Seq primer: SK.

## FEATURES

location/Qualifiers  
 1..95  
 /organism="Schistosoma mansoni"  
 /strain="Egyptian"  
 /db\_xref="taxon:6183"  
 /clone="SMTBADAMS0038SK"  
 /clone\_lib="S. mansoni cDNA"  
 /lab\_host="E. coli XL Blue"  
 /note="Vector: pBluescript II SK+; Site-1: EcoRI; Site-2: XhoI; mRNA was purified from adult couples of S. mansoni. cDNA was constructed and cloned simultaneously using vector priming with the pBluescript II SK+ vector. cDNA was directionally synthesized from the EcoRI site in the vector to the XhoI site."  
 BASE COUNT  
 31 a 15 c 10 g 39 t

## BASE COUNT

31 a 15 c 10 g 39 t

## ORIGIN

Query Match 0.5%; Score 26.4; DB 14; Length 95;  
 Best Local Similarity 59.2%; Pred. No. 6.5e+04;  
 Matches 45; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

## QY 641

ACCTCTTTTATATACAGCCCTCAAGCCATCCAGATATATTAATGAATCCTACTT 700  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 5 ACATATATATATATATACATAGTTCAGCATCCCTTATATTAATGAATCCTACTT 64  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 701 TCAAGTCGATATG 716  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 65 TGAATTTTACCATAG 80

## RESULT 21

R40354/c  
 LOCUS Y81d05.s1 Soares infant brain INIB Homo sapiens cDNA clone  
 DEFINITION IMAGE:29017 3', mRNA sequence.  
 R40354  
 VERSION R40354.1 GI:797970  
 KEYWORDS EST.  
 SOURCE Human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 78)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Holman  
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
 Rifkin, L., Rohlfing, T., Soares, M., Ten, F., Trevisakis, E., Waterston  
 R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The Wash-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson R.  
 Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 2347  
 High quality sequence stops: 61 Source: IMAGE Consortium, LNL, This  
 clone is available royalty-free through LNL; contact the IMAGE  
 Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 2347 Std Error: 0.00  
 Seq primer: Promega -21ml3  
 High quality sequence stop: 48.

## FEATURES

location/Qualifiers  
 1..78  
 /organism="Homo sapiens"  
 /db\_xref="GDB:401364"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:29017"  
 /clone\_lib="Soares infant brain INIB"  
 /sex="female"  
 /dev\_stage="73 days post natal"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Organ: whole brain; Vector: Lactid BA; Site-1: Not I; Site-2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' AATCGAAGATTGCGCGCCGCAATATTTTATTAAGTCCCTAC 3') double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lactid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."  
 BASE COUNT  
 7 a 5 c 7 g 57 t 2 others

Query Match 0.5%; Score 26.2; DB 14; Length 78;  
 Best Local Similarity 64.9%; Pred. No. 6.9e+04;  
 Matches 37; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 498 AAGCTTACCTGCTCAAGAAAAAAGACAGGACCAAGAGCAAGAAAAATAC 554

Db 78 AGAGTGNAACTCTGCTCAAAAAAAAAAAAAAAAAANAAAAAAAAACAAGAC 22

RESULT 22	LOCUS	DEFINITION
AV551027	93 bp	linear EST 06-SEP-2000
AV551027	Arabidopsis thaliana roots	Columbia Arabidopsis thaliana
CDNA clone R2120D09R 5',	mrna sequence.	

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5393853"
/clone_id="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: breast; Vector: PCMV-SPOrt6; Site:1: NotCl; Site:2: Salt; Cloned unidirectionally, oligo-dT primed. Average insert size 1,383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."

```

Query Match	0.58;	Score 26;	DB 13;	Length 78;
Best Local Similarity	59.58;	Pred. No. 7.8e+04;		
Matches	44;	Conservative	0;	Mismatches 30;
			Indels	0;
			Gaps	0

Accession	Sequence	Position
Y	ATGGTCCACCGGACATTAAAGTGCACAAATCTTCCCTTACCTCATCTGGATTATACAA	4083
Db	2 ATCATCACCAGGAGATGTGAAGCCCTCCACATCTCTGTAACCTAGAGGGGAGATCAAG	61
Qy	CTGGAGATTTCG 4097	
Db	62 CTGTGTGACTTCGG 75	

RESULT 25	LOCUS	DEFINITION	ACCESSION
BH127076/C	BH127076	85 bp DNA G-10g24.f Maize Random Small-insert Genomic Library Zea mays genomic clone G-10g24 both, DNA sequence.	GSS 23-JUL-2001 BH127076

VERSION	BH127076.1	GI:14994908
KEYWORDS	GSS.	
SOURCE	Zea mays.	
ORGANISM	Zea mays	

REFERENCE

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 85)

AUTHORS	Meyers, B. C., Tingey, S. V. and Morgante, M.
TITLE	Abundance, distribution and transcriptional activity of repetitive elements in the maize genome
JOURNAL	Genome Res. 11 (10), 1660-1676 (2001)
MEDLINE	21475670
COMMENT	Contact: Morgante M

Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com  
Sequences were trimmed to include only high quality bases: forward  
and reverse reads were assembled when significant overlaps were  
detected.  
Seq primer: M13univ  
Class: shotgun.

```

FEATURES
      source
            Location/Qualifiers
              1..85
                /organism="Zea mays"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="G-10g24"
                /clone_lib="Maize Random Small-Insert Genomic Library"
                /sex="hermaphrodite"
                /tissue_type="leaf"
                /cell_type="Young leaf"
                /dev_stage="seedling"
                /note="Vector: pCR-script; Total genomic DNA was nebulized
                        ; ends were polished with Pfu polymerase and the fragments
                        cloned into pCR-script."
              20 a
                  18 c
                      11 g
                          36 t

```

ORIGIN	Query Match	0.5%	Score 26;	DB 17;	Length 85;
	Best Local Similarity	57.3%		Pred. No. 8.1e+04;	
	Matches	47;	Conservative	0;	Mismatches 35; Indels 0; Gaps 0;
QY	186	AAAAACAGTGGAGAATGTGGAAAGATATACAGCTATACAGCAGAGAGAAAAAGATCCGAGCAGC	245		
Db	84	AAACATCAATGAGGGGCAAGCGTGGGCCAAATTTTAATATACAGAGAAAAACAATCCACACATA	25		
QY	246	TCTTACAAACAAGAGCGTGAT	267		
Db	24	TCTTATGAAGAGATAAATTGGT	3		

RESULT 26	AA865746	88 bp	mRNA	linear	EST 13-MAY-1998
LOCUS	AA865746				
DEFINITION	AA865746				
ACCESSION	AA865746				
VERSION	AA865746				
KEYWORDS	AA865746.1	GI:2958022			
SOURCE	EST.				
	human.				

ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL	COMMENT
Homo sapiens			
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:			
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.			
1 (bases 1 to 88)			
NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .			
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
Tumor Gene Index			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmett-Buck, M.D., Ph.D.  
CDNA Library Arrayed by: M. Bento Soares, Ph.D.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Clone distribution by: Washington University Genome Sequencing Center  
founded through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.linnl.gov/bbrp/image/image.html](http://www.bio.linnl.gov/bbrp/image/image.html)  
Insert length: 2310 Std Error: 0.00  
Seq primer: -40m13 fwd. Err from Amersham  
High quality sequence stop: 51.  
Location/Qualifiers:

```

source
1. 88
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1 IMAGE:1469253"
/clone_1b="NCI CGAP GC4"
/tissue_type="pooled germ cell tumors"
/lbs.host="DH10B"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
31 a 10 c 13 g 34 t

```

Query Match	0.58;	Score 26;	DB 9;	Length 88;
Best Local Similarity	62.13;	Pred. No. 8.2e+04;		
Matches 41;	Conservative	0;	Mismatches 25;	Indels 0;
				Gaps 0;
643	TTCTTTTATATACAGCCCGCAAGCANC	CCCGCATTTATTTAAAGAAATCCTTACTTC	702	
23	TACTTTATATACAAATGGTGAAGTGTGAC	AAAGTTTGATATATACGTGAAGCCATACCTTC	82	
703	AAAGTC	708		



Location/Qualifiers

adenocarcinoma tissue, cDNA made by oligo-dT priming.

BASE COUNT	Directionally cloned, Size-selected on agarose gel, average insert size 400 bp. Primary library, non-amplified."			
ORIGIN	39 a	7 c	35 g	10 t

	Query Match	0.5%	Score 25.8;	DB 9;	Length 91;
	Best Local Similarity	58.4%	Pred. No.	9.4e+04;	
	Matches    4;	Conservative	0;	Mismatches    32;	Indels         0;
				Gaps              0;	
Oy	1115 AGCCCGACTATAGGGGTGCACAGCAGGAGATTAAAGCACTGTAGTTCGG	1174			
Dd	5 AGAAGCACAGACAGGACGAGTGACAAGAAGTAGTAAGTGACAGAGGAGGAACAATGCCGCTG	64			
Oy	1175 ATGAGAGTTGAAGAAGAA	1191			
Dd	65 AGGTGGAGAGAAGAAAAA	81			

RESULT 32	91 bp	mrna	linear	EST 27-JUL-1999
AI89A187/c				
LOCUS				
DEFINITION				
AI89A187				
mc76e06.x1 Soares mouse embryo NM013.3 14.5 Mus musculus cDNA				
clone IMAGE:353602 3 similar to SW:RPB2.HUMAN P0876 DNA-DIRECTED				
RNA POLYMERASE II 140 KD POLYPEPTIDE ; ; mRNA sequence.				

ACCESSION	A1894187	
VERSION	A1894187.1	GI:5600089
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

**REFERENCE**  
(bases 1 to 91)  
**AUTHORS** Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepec, M., Theising, B., Allen, M., Bowers, J., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritten, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
**TITLE** The WashU-NCI Mouse ESR Project 1999  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Marra M/WashU-NCI Mouse ESR Project 1999  
Department of Medicine  
School of Medicine

Email: mousesteel@watson.wustl.edu  
This clone is available royalty-free through LLN<sup>1</sup>; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 3' end only. This new data is from the 3' end  
trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
High quality sequence: stop...1.

```

1. 91
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:353602"
/clone_1fb="Scaris mouse embryo NBME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/notes="Vector: p7773D-pac (Pharmacia) with a modified
polylinker. Site:1: Not I, oligo(dT) primer 15',
5'-TGTTCACATCTGGAAGGAGGAGCGCGCGAGATATTTTGTGTGTGTGT
T3'1', on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
Eco RI sites of the modified

```

BASE COUNT  
ORIGIN

25 a	19 c	14 g	33 t
------	------	------	------

	Query Match	0.5%	Score 25.8;	DB 9;	Length 91;	
	Best Local Similarity	67.9%;	Pred. No.	9.4e+04;		
	Matches	36;	Mismatches	17;	Indels	0;
					Gaps	0;
OY	1381	CCATTGTAGCAACGACATGAGCGATGGGTTAAGAACTTAATTTAAG	1433			
DB	63	CCACTGGAAACCACCGTTCCTCAGAAATATGGGATAAACCAAATCATTTATAG	11			

RESULT 33					EST 27-JUN-2002
AL794139/c					
LOCUS	100 bp	mrna	linear		
AL794139					
DEFINITION	XGC-neurula	Slurana tropicalis	cdna clone	TNeu116m13	5',
	mrna sequence.				

ACCESSION AL794139  
VERSION AL794139.1 GI:21579843  
KEYWORDS  
SOURCE ESR.  
ORGANISM western clawed frog.  
Silurana tropicalis  
Morphology: Metamorpho: Chordata: Vertebrata: Euteleostomi:

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (basses 1 to 100)  
Taylor, R., Ashurst, J. L., Cronling, M. D. R., Zorn, A. M. and Rogers, J  
Sander Xenopus tropicalis EST project 2002  
Unpublished (2001)  
Contact: Taylor R

Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK  
Email: trop@sanger.ac.uk  
Sanger Xenopus tropicalis EST project 2001  
TROPICALIS\_SEQUENCE\_ID: TNEu116m3.p1csp6  
Sequencing primer from a Xenopus gene collection (XGC) library  
This sequence is from a Xenopus M. zorn.  
constructed by Aaron M. Zorn.

```

FEATURES
SOURCE
    LOCATOR/GeneID/LOC
    1. 100
    /organism="Silviana tropicalis"
    /db_xref="taxon:8364"
    /clone_1b="Neull6m13"
    /clone_1b="XGC-neurula"
    /dev_stage="neurula"
    /db_xref="Escherichia coli DH10B"
    /note="vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
BASE COUNT
    17 a 15 c 18 g 50 t
ORIGIN

```

		0.54;	Score 25.8;	DB 9;	Length 100;
Query Match			Pred. No. 9,	7e+04;	
Best Local Similarity	67.9%;		Mismatches 17;	Gaps 0;	
Matches 36;	Conservative	0;			
Oy	505	ACCTCAGTCTCAAGAAAAAAGACGAGGAGGAAGAAGACACAGAAATACGTC	557		
Dd	73	AGCTCGCTTAATAAACACAAAACAAAAGACAACAAAAAATAATATC	21		
RESULT 34					
A1142956			73 bp	mRNA	linear
LOCUS	A1142956				Estr 25-SHP-1996
DEFINITION	oz58dd01.x1			Sources: senescent fibroblasts NBHSP Homo sapiens cDNA	
DESCRIPTION	clone IMAGE:1679621 3'			similar to SW:SF54.HUMAN P13624 SIGNAL	
RECOGNITION	PARTICLE 54			KD PROTEIN ; , mRNA sequence.	
ACCESSION	A1142956				
VERSION	A1142956.1			GI:3659315	

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 73)
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997)
CONTACT	Contact: Robert Strausberg, Ph.D.

FEATURES	source
High quality sequence stop: 1.	1. '73
Seq primer: 40m13 fwd. ET from AmerSham	
IMAG Consortium (info@image.llnl.gov) for further information.	
This clone is available royalty-free through LNL ; contact the	
Email: c9apbs-r@mail.nih.gov	
Contact: Robert Strausberg, Ph.D.	
undeposited (1997)	
COMMENT	

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_1="IMAGE:1679521"  
 /clone\_1b="Soares senescent fibroblasts\_NBHSF"  
 /tissue\_type="senescent fibroblasts"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Vector: pP73b (pharmacia) with a modified  
 polylinker V-type: phagemid; Site\_1: Not I; Site\_2: Eco RI  
 primer 1: 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer 15"  
 TGTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'},  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pP73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo."

Query Match	0.5%	Score 25.6	DB 9	Length 73
Best Local Similarity	62.5%	Pred. No. 9.8e+04		
Matches 40	Conservative 0	Mismatches 24	Indels 0	Gaps 0
QY	1632	ATTGGAACCGCCTTCCTAGTCTCTGCGCAGTCCCTTGAATGATCATGATGAGTGTCT	1691	
Db	10	ATTTCATTCATGCTTTTCATGTTCGACGACGACCCCTGTGAACCTGCCTTATCAGTACT	69	
QY	1692	GAAG	1695	
Db	70	GAAG	73	

RESULT		35				
A1086378/c						
LOCUS						
DEFINITION	A1086378	85 bp	mRNA	linear	EST 01-OCT-1998	
	GZ44G.C01.x1	Sources_NHMPU_ST Homo sapiens	CDNA clone IMAGE:1678176			
ACCESSION	A1086378					
VERSION	A1086378					
KEYWORDS	A1086378.1	GI:3424801				
SOURCE	human.					

ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL COMMENT
Homo sapiens	Elkayots; Melazzo; Chordata; Cranata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 85)	
NCI-CGAP	<a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
Unpublished (1997)		
Contact: Robert Strausberg, Ph.D.		
Email: <a href="mailto:cgapds-remail.nih.gov">cgapds-remail.nih.gov</a>		
This clone is available royalty-free through LNL ; contact the IMAGE Consortium ( <a href="mailto:info@imgl.lnl.gov">info@imgl.lnl.gov</a> ) for further information.		
Insert Length: 1214	Std Error: 0.00	

FEATURES	
Seq primer: -40m13 fwd. ET from Amersham	
High quality sequence stop: 62.	
Location/Qualifiers	
source	1. .85

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1678176"
/clone_lib="Scorers.NHMPu-S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/notes="Organ: mixed (see below): Vector: pT73D-Pac
(pharmacia) with a modified polylinker: Site.1: Not I;
Site.2: Eco RI: Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHn, pregnant uterus
NBHNPu, and fetal heart NBHNI9w) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

```

	Query Match	0.5%	Score 25.6;	DB 9;	Length 85;
	Best Local Similarity	57.5%;	Pred. No. 1e+05;		
	Matches	46;	Conservative	0;	Mismatches 34;
					Indels 0;
					Gaps 0;
Qy	472	TTTTTTGAACCTTTTCACGCTTTTGGTAAGCTTACCTCAGTCTCAAAAGAAAAAGACAGG	531		
Db	81	TTTTTACGGGTTCCCAAAATTAATAATATGTAAACCAAGTCAAAAAATTAATAATAA	22		
Qy	532	GAGCAAAAGAGGACAAAGAAA	551		
		-		-	
		-		-	
Db	21	AAAAAAAAAAAAAAAAAAAAA	2		

RESULT 36	
AV532477	
LOCUS	86 bp mRNA linear
DEFINITION	AV532477 Arabidopsis thaliana flower buds Columbia
ACCESSION	thaliana cDNA clone FB042h01F 3', mRNA sequence.
VERSION	AV532477
KEYWORDS	AV532477.1 GI:8692760
SOURCE	EST.
ORGANISM	thale cress.
	Arabidopsis thaliana

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

Kosida; eutrods II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 86)  
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7, 175-180 (2000)  
20363093  
Contact: Erika Asamizu

FEATURES

SOURCE

1. 86

/organism="Arabidopsis thaliana"  
/strain="Columbia"  
/db\_xref="taxon:3702"  
/clone="PB042H01F"  
/clone\_lib="Arabidopsis thaliana flower buds Columbia"  
/tissue\_type="flower buds"  
/note="Vector: pBluescriptII SK-, Site\_1: EcoRI; Site\_2: XhoI"

The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: [asami@kazusa.or.jp](mailto:asami@kazusa.or.jp), URL: <http://www.kazusa.or.jp/en/plant/>.



RESULT	39
AZ961698/c	
LOCUS	89 bp DNA linear GSS 27-APR-2001
DEFINITION	2M0230B17F Mouse 10kb plasmid U05C2M library Mus musculus genomic
ACCESSION	clone U05C2M0230B17 F, DNA sequence.
VERSION	AZ961698
	GI:13832925

KEYWORDS GSS.  
SOURCE Mus musculus.  
ORGANISM house mouse.  
REFERENCE 1 (bases 1 to 89)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,  
'M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.  
and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0230 row: B column: 17  
Seq primer: CGTGTAAACGACGCGCCACG  
Class: plasmid ends  
FEATURES  
High quality sequence stop: 89.  
location/Qualifiers  
1..89

BASE COUNT	28 a	17 c	16 g	28 t
ORIGIN				

Query Match	0.5%;	Score 25.4;	DB 17;	Length 89;
Best Local Similarity	58.7%;	Pred. 0.1,2e+05;		
Matches 44;	Conservative	0;	Mismatches 31;	Indels 0;
				Gaps 0;
OY	4054	ATCTTCCTTACCTTCATCTGATTTATCAACCTGGAGATTTTGGATGTTCAAGTAAAGTC	4113	
Db	88	ATATTTTCAACCAAGATGCAACAGTCGAGCTTGAGATTTTGGAAITTGCTCCAGTTCTT	29	
OY	4114	AAAAACATGCCCCAG	4128	
Db	28	AATAGCTTAACACAG	14	

RESULT 40			
D19910			
LOCUS	D19910	91 bp	mRNA linear EST 30-JUL-1996

DEFINITION	HUMGSO0867 Human promyelocyte Homo sapiens cDNA clone mm0905 3', mRNA sequence.
ACCESSION	D19910
VERSION	D19910.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinaiti,H., Arimoto,J. and Matsubara,K.
TITLE	Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed cDNA sequencing (1993)
JOURNAL	Unpublished (1993)
COMMENT	Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinaiti,H., Arimoto,J. and Matsubara,K. Institute for Molecular and Cellular Biology Osaka University 3-1 Yamada-oka,Suita,Osaka 565,Japan.
FEATURES	
SOURCE	1..91 Location/Qualifiers

BASE COUNT	32 a	15 c	20 g	24 t
ORIGIN				

	Query Match	0.5%	Score 25.4	DB 14	Length 91
	Best Local Similarity	68.6%	Pred. No. 1.2e+05		
	Matches	35	Conservative	0	Mismatches 16; Indels 0; Gaps 0
OY	4936	TGCAATTAAAGAAAAGCTTCCTTTTTCATTAATAATGGTTATTTTACGAAA	4986		
Dd	41	TGACACTTAAGAATTAATTTGGTTGGTAGTAATAAAGCGCTTGCTGCAGAAA	91		

Search completed: November 11, 2002, 10:46:34  
Job time : 4287 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 05:35:07 ; Search time 630 Seconds  
(without alignments)  
17837.257 Million cell updates/sec

Title: US-09-676-436-3  
Perfect score: 4990  
Sequence: 1 ctgaagactctccgatga.....ggtattatctgaagactc 4990

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2389434

Minimum DB seq length: 8  
Maximum DB seq length: 100

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database :  
1: N\_Geneseq\_101002.\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
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13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
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20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	1.2	60	24	ABN55465
2	44.8	0.9	65	24	ABN55582
3	28	0.6	78	24	AAD37143
4	27.2	0.5	28	18	AA750934
5	26.6	0.5	92	21	AAAC19445
6	26	0.5	26	24	AAD37145
7	26	0.5	100	16	AA086400
8	25.8	0.5	81	24	ABK55302
9	25.2	0.5	60	22	AAH46893

10	25.2	0.5	70	21	AAA71594	Human brain natrin
11	25.2	0.5	89	16	AAT22086	Human gene signatu
12	25.2	0.5	99	18	AAT92244	Mercuric ion reduc
13	25.2	0.5	99	20	AA228594	Primer 307-3395 fo
14	25.2	0.5	54	21	AAA73946	GFP Leu(CTG)5 forw
15	25	0.5	91	22	ABA69691	Human foetal olig
16	25	0.5	96	24	ABL58788	Synthetic GFP olig
17	24.8	0.5	77	22	AAAC12392	Human secreted pro
18	24.8	0.5	92	21	AA506930	Reverse PCR primer
19	24.8	0.5	94	21	AAAC1499	Human secreted pro
20	24.8	0.5	94	21	AAAC1541	Human secreted pro
21	24.8	0.5	65	24	ABN54107	Mouse spliced tran
22	24.6	0.5	71	18	AA655208	Transforming growt
23	24.6	0.5	72	21	AA523348	cDNA encoding Dros
24	24.6	0.5	72	21	AA523348	HCY DNA encoding H
25	24.6	0.5	98	20	ABK34658	Human neutrophil c
26	24.4	0.5	82	20	AAK23428	80Kc Bundle peptid
27	24.4	0.5	99	22	ABK35588	Human foetal liver
28	24.4	0.5	99	22	ABK35588	Human foetal liver
29	24.4	0.5	100	16	AA086411	Probe #14054 for g
30	24.2	0.5	80	22	AAK72801	Human insulin deri
31	24.2	0.5	80	22	AAK21231	Human foetal liver
32	24.2	0.5	80	22	AAK47388	Human brain expres
33	24.2	0.5	80	22	AAK47388	Human brain expres
34	24.2	0.5	84	21	AAA92397	Human bone marrow
35	24.2	0.5	90	24	ABK36388	Probe #21912 used
36	24.2	0.5	94	21	AAH51645	HIV DNA encoding G
37	24.2	0.5	94	21	AAH51645	Sbgl exon sequence
38	24.2	0.5	94	21	AAH51692	Sbgl exon sequence
39	24.2	0.5	95	22	ABA71915	Human foetal liver
40	24.2	0.5	95	22	AAK20302	Human brain expres
41	24.2	0.5	95	22	AAK46381	Human bone marrow
42	24.2	0.5	95	22	AA152270	Probe #20956 used
43	24.2	0.5	95	22	AA152270	Human genome deriv
44	24.2	0.5	99	22	ABA73946	Human foetal liver
45	24.2	0.5	99	22	ABA73946	Human foetal liver
46	24.2	0.5	98	22	AAK39875	Probe #18368 for g
47	24.2	0.5	98	22	AAK39875	Human brain expres
48	24.2	0.5	99	22	AAK26980	Human bone marrow
49	24.2	0.5	99	22	AAK26980	Human bone marrow
50	24.2	0.5	99	22	AAK26980	Human bone marrow
51	24.2	0.5	99	22	AAK26980	Human bone marrow
52	24.2	0.5	99	22	AAK26980	Human bone marrow
53	24.2	0.5	99	22	AAK26980	Human bone marrow
54	24.2	0.5	99	22	AAK26980	Human bone marrow
55	24.2	0.5	99	22	AAK26980	Human bone marrow
56	24.2	0.5	99	22	AAK26980	Human bone marrow
57	24.2	0.5	99	22	AAK26980	Human bone marrow
58	24.2	0.5	99	22	AAK26980	Human bone marrow
59	24.2	0.5	99	22	AAK26980	Human bone marrow
60	24.2	0.5	99	22	AAK26980	Human bone marrow
61	24.2	0.5	99	22	AAK26980	Human bone marrow
62	24.2	0.5	99	22	AAK26980	Human bone marrow
63	24.2	0.5	99	22	AAK26980	Human bone marrow
64	24.2	0.5	99	22	AAK26980	Human bone marrow
65	24.2	0.5	99	22	AAK26980	Human bone marrow
66	24.2	0.5	99	22	AAK26980	Human bone marrow
67	24.2	0.5	99	22	AAK26980	Human bone marrow
68	24.2	0.5	99	22	AAK26980	Human bone marrow
69	24.2	0.5	99	22	AAK26980	Human bone marrow
70	24.2	0.5	99	22	AAK26980	Human bone marrow
71	24.2	0.5	99	22	AAK26980	Human bone marrow
72	24.2	0.5	99	22	AAK26980	Human bone marrow
73	24.2	0.5	99	22	AAK26980	Human bone marrow
74	24.2	0.5	99	22	AAK26980	Human bone marrow
75	24.2	0.5	99	22	AAK26980	Human bone marrow
76	24.2	0.5	99	22	AAK26980	Human bone marrow
77	24.2	0.5	99	22	AAK26980	Human bone marrow
78	24.2	0.5	99	22	AAK26980	Human bone marrow
79	24.2	0.5	99	22	AAK26980	Human bone marrow
80	24.2	0.5	99	22	AAK26980	Human bone marrow
81	24.2	0.5	99	22	AAK26980	Human bone marrow
82	24.2	0.5	99	22	AAK26980	Human bone marrow

Human brain natrin  
Human gene signatu  
Mercuric ion reduc  
Primer 307-3395 fo  
GFP Leu(CTG)5 forw  
Human foetal olig  
Synthetic GFP olig  
Human secreted pro  
Reverse PCR primer  
Human secreted pro  
Human secreted pro  
Mouse spliced tran  
Transforming growt  
cDNA encoding Dros  
HCY DNA encoding H  
80Kc Bundle peptid  
Human foetal liver  
Human foetal liver  
Human insulin deri  
Human foetal liver  
Human brain expres  
Human brain expres  
Human bone marrow  
Probe #21912 used  
HIV DNA encoding G  
Sbgl exon sequence  
Sbgl exon sequence  
Sbgl exon sequence  
Human foetal liver  
Human brain expres  
Human bone marrow  
Probe #20956 used  
Human genome deriv  
Human foetal liver  
Human foetal liver  
Probe #18368 for g  
Human brain expres  
Human bone marrow  
Human bone marrow  
Probe #16913 for g  
Probe #24684 used  
Human MEK4 DNA am  
Human spliced tran  
Mouse spliced tran  
Synthetic transect  
Cell death protect  
Clone 92-2 used, in  
SSP 5.11.11.5 clon  
Synthetic storage  
Human SNP oligonuc  
Human SNP oligonuc  
Mouse spliced tran  
Expression vector  
Human foetal liver  
Probe #15434 for g  
Human brain expres  
Human bone marrow  
Probe #14775 for g  
Probe #19061 used  
Human genome-deriv  
Sequence encoding  
Human gene signatu  
Coupled ligation a  
Coupled ligation a  
Human G-protein su  
Human spliced tran  
Human gene signatu  
Mouse spliced tran  
Mouse spliced tran  
Human secreted pro  
Human secreted pro  
Coupled ligation a

83	23.6	0.5	99	22	AAF32800	Serine protease in
84	23.4	0.5	51	22	AAI32250	Human SNP oligonuc
C 85	23.4	0.5	54	21	AAAT3932	GFP Gln(CAG)5 forw
C 86	23.4	0.5	83	22	AAS23479	C. albicans essent
C 87	23.4	0.5	84	16	AAAT23872	Human gene signatu
C 88	23.4	0.5	98	21	AAC28690	Human secreted pro
C 89	23.4	0.5	99	21	AAZ32903	Streptococcus pyog
C 90	23.2	0.5	60	24	ABN32994	Human spliced tran
C 91	23.2	0.5	60	24	ABN44856	Human spliced tran
C 92	23.2	0.5	65	24	ABN28668	Human spliced transc
C 93	23.2	0.5	65	24	ABN30979	Rat spliced transc
C 94	23.2	0.5	91	16	AAT25335	Human gene signatu
C 95	23.2	0.5	93	21	AAAI0072	Oligonucleotide OA
C 96	23.2	0.5	93	22	ABA49862	Human breast cell
C 97	23.2	0.5	93	22	ABA67781	Human foetal liver
C 98	23.2	0.5	93	22	ABA34838	Human foetal liver
C 99	23.2	0.5	93	22	AAK16192	Human brain expres
100	23.2	0.5	93	22	AAK14936	Human bone marrow
101	23.2	0.5	93	22	AAK122704	Probe #12637 for g
102	23.2	0.5	93	22	AAI47999	Probe #16685 used
103	23.2	0.5	93	22	AAI08366	Probe #8357 used t
104	23.2	0.5	93	22	ABSI08366	Human genome-deriv
105	23.2	0.5	94	21	AAHS1567	Sbgl exon sequence
C 106	23.2	0.5	96	22	ABA71064	Human foetal liver
C 107	23.2	0.5	96	22	AAK19348	Human brain expres
C 108	23.2	0.5	96	22	AAK45327	Human bone marrow
C 109	23.2	0.5	96	22	AAK6344	Human bone marrow
C 110	23.2	0.5	96	22	AAI51280	Probe #19966 used
C 111	23.2	0.5	96	24	ABSI19585	Human genome-deriv
112	23.2	0.5	97	22	ABA515204	Human foetal liver
113	23.2	0.5	97	22	ABA39867	Probe #18333 for g
114	23.2	0.5	97	22	ABA59824	Human brain expres
115	23.2	0.5	97	22	AAK23739	Human bone marrow
116	23.2	0.5	97	22	AAK49838	Probe #16876 for g
117	23.2	0.5	97	22	AAI25953	Probe #24439 used
118	23.2	0.5	97	24	ABS23338	Human genome-deriv
C 119	23.2	0.5	97	21	AAI5527	Human secreted pro
C 120	23.2	0.5	47	21	AAZ67744	Human map-related
C 121	23.2	0.5	60	21	AAAS3688	Oligonucleotide us
C 122	23.2	0.5	65	24	ABN28820	Rat spliced transc
123	23.2	0.5	65	24	ABN28860	Rat spliced transc
124	23.2	0.5	65	24	ABN28860	Mouse spliced tran
C 125	23.2	0.5	84	22	ABNS3179	Human breast cell
C 126	23.2	0.5	84	22	ABA51576	Human foetal liver
C 127	23.2	0.5	84	22	ABA40656	Probe #19122 for g
C 128	23.2	0.5	84	22	AAK24775	Human brain expres
C 129	23.2	0.5	84	22	AAK50772	Human bone marrow
C 130	23.2	0.5	84	22	AAI27789	Probe #17722 for g
C 131	23.2	0.5	84	22	AAI56761	Probe #25447 used
C 132	23.2	0.5	86	21	AAC31907	Human genome-deriv
133	23.2	0.5	86	21	AAC31907	Human secreted pro
134	23.2	0.5	90	22	ABAI8123	Human nervous syst
135	23.2	0.5	90	22	AAAS40420	DNA encoding human
136	23.2	0.5	90	22	AAI04023	Human immunoprolife
137	23.2	0.5	90	22	AAK86864	Human immune/haema
C 138	23.2	0.5	90	22	AAK86864	Human immune/haema
C 139	23.2	0.5	91	22	AAI45354	Strept-tag PCR prim
C 140	23.2	0.5	94	20	AAI17882	Human brain expres
C 141	23.2	0.5	94	21	AAZ57911	Fuzzy Csd gene fra
C 142	23.2	0.5	95	22	AAI470725	Human foetal liver
C 143	23.2	0.5	95	22	AAK18973	Human foetal liver
C 144	23.2	0.5	95	22	AAK44923	Human brain expres
C 145	23.2	0.5	95	22	AAI50894	Human bone marrow
C 146	23.2	0.5	95	24	ABSI19165	Probe #19580 used
147	23.2	0.5	95	24	ABK36955	Human genome-deriv
148	22.8	0.5	100	24	AAI27481	HIV subcasette PC
149	22.8	0.5	51	22	ABN41391	Human SNP oligonuc
C 150	22.8	0.5	60	24	ABN44406	Human spliced tran
C 151	22.8	0.5	60	24	ABN44406	Human spliced tran
C 152	22.8	0.5	65	24	ABN31577	Rat spliced transc
C 153	22.8	0.5	87	22	ABA76706	Human foetal liver
C 154	22.8	0.5	87	22	AAK51343	Human bone marrow
C 155	22.8	0.5	87	22	AAI57410	Probe #26096 used
C 156	22.8	0.5	87	24	ABS24888	Human genome-deriv
156	22.8	0.5	87	24	AAS98534	Human protective D
C 157	22.8	0.5	89	22	AAI47772	Probe #18458 used
C 158	22.8	0.5	90	24	AAK36526	HCV DNA encoding H
C 159	22.8	0.5	94	22	AAAF6813	Codon-optimised HP
160	22.8	0.5	95	12	AAQ10538	Non-A non-B hepariti
161	22.8	0.5	95	13	AAO25213	NANBH probe in lam
C 162	22.8	0.5	95	21	AAAS5088	Rat genomic DNA ve
C 163	22.8	0.5	96	18	AAI49235	HVRI region of E2
C 164	22.8	0.5	98	21	AAC33251	Human secreted pro
C 165	22.8	0.5	100	20	AAK57267	Human ROBO1 hybrid
166	22.8	0.5	51	22	AAI77908	Human silent SNP c
C 167	22.6	0.5	51	22	AAI77910	Human silent SNP c
C 168	22.6	0.5	51	22	AAH69796	Human coding sequ
C 169	22.6	0.5	60	24	ABN38012	Human spliced tran
C 170	22.6	0.5	64	24	ABK55167	Human colon cancer
171	22.6	0.5	64	24	ABNS5782	Mouse spliced tran
172	22.6	0.5	65	24	ABN5782	Human secreted pro
173	22.6	0.5	80	21	AAC19848	Bovine embryonic g
174	22.6	0.5	84	24	ABN73404	Sbgl exon sequence
175	22.6	0.5	94	21	AAHS1680	Human foetal liver
176	22.6	0.5	98	22	ABAT3670	Probe #17361 for g
177	22.6	0.5	98	22	ABA38895	Human bone marrow
178	22.6	0.5	98	22	AAK22117	Human brain expres
179	22.6	0.5	98	22	AAK48284	Human bone marrow
180	22.6	0.5	98	22	AAI54109	Probe #22795 used
181	22.6	0.5	98	22	ABS22147	Human genome-deriv
182	22.6	0.5	100	22	ABAT5776	Human foetal liver
183	22.6	0.5	100	22	ABAA0347	Probe #18613 for g
184	22.6	0.5	100	22	AAK50450	Human bone marrow
185	22.6	0.5	100	22	AAI27464	Human bone marrow
186	22.6	0.5	100	22	AAI56433	Probe #17397 for g
187	22.6	0.5	100	24	ABS23922	Probe #25119 used
188	22.6	0.5	100	24	ABK29699	Human genome-deriv
C 189	22.4	0.4	56	18	AAAT61791	Colon adenocarcino
C 190	22.4	0.4	60	24	ABN38133	Oligonucleotide
C 191	22.4	0.4	65	24	ABN29626	Human spliced tran
C 192	22.4	0.4	65	24	ABNS5412	Rat spliced transc
C 193	22.4	0.4	65	24	ABNS5412	Mouse spliced tran
C 194	22.4	0.4	76	22	AAI26154	Human breast cance
195	22.4	0.4	87	21	AAI18326	Human secreted pro
196	22.4	0.4	94	16	AAAT2073	Human gene signatu
197	22.4	0.4	95	15	AAO95215	Simple tandem repe
198	22.4	0.4	95	22	ABA49080	Human breast cell
199	22.4	0.4	95	22	ABA66992	Human foetal liver
200	22.4	0.4	95	22	ABA34083	Probe #12549 for g
201	22.4	0.4	95	22	AAK15438	Human brain expres
202	22.4	0.4	95	22	AAK41165	Human bone marrow
203	22.4	0.4	95	22	AAI21925	Probe #11858 for g
204	22.4	0.4	95	22	AAI47211	Probe #15897 used
205	22.4	0.4	95	22	AAI07613	Probe #7604 used t
206	22.4	0.4	95	24	ABSI15171	Human genome-deriv
207	22.4	0.4	97	14	AAO37272	Clone D33 used in
208	22.4	0.4	97	14	AAO37275	Clone 86-H23 used
209	22.4	0.4	97	16	AAAT26728	Human gene signatu
210	22.4	0.4	97	16	AAO94994	SSP 5.8.8.5 clone
211	22.4	0.4	97	16	AAV35832	Synthetic storage
C 212	22.4	0.4	100	22	AAV99529	Synthetic storage
C 213	22.4	0.4	100	22	ABA70538	Human foetal liver
C 214	22.4	0.4	100	22	AAK18782	Human brain expres
C 215	22.4	0.4	100	22	AAK44719	Human foetal liver
C 216	22.4	0.4	100	22	AAI50697	Human bone marrow
C 217	22.2	0.4	100	22	ABSI8957	Probe #19383 used
218	22.2	0.4	51	22	AAI78853	Human genome-deriv
219	22.2	0.4	51	22	ABL00753	Human silent SNP c
C 220	22.2	0.4	60	24	ABN36495	Human amino acid c
221	22.2	0.4	60	24	ABN40287	Human spliced tran
222	22.2	0.4	60	24	ABN30319	Human spliced tran
223	22.2	0.4	60	24	ABN50457	Human spliced tran
224	22.2	0.4	60	24	ABN58633	Human spliced tran
C 225	22.2	0.4	65	24	ABN27354	Rat spliced transc
C 226	22.2	0.4	65	24	ABN28879	Rat spliced transc
C 227	22.2	0.4	65	24	ABN30888	Rat spliced transc
C 228	22.2	0.4	71	18	AAI55371	Human keratinocyte
C 229	22.2	0.4	73	18	AAV75907	Staphylococcus aur

C 229	22.2	0.4	75	22	ABAT3674	Human foetal liver	302	21.8	0.4	72	22	AA51198	Antibody variable
C 230	22.2	0.4	75	22	ABAT3898	Probe #17364 for g	C 303	21.8	0.4	77	24	ABK54849	Human colon cancer
C 231	22.2	0.4	75	22	AAK22121	Human brain expres	C 304	21.8	0.4	78	13	AAQ21847	PEX2A/II (Asp15->A
C 232	22.2	0.4	75	22	AAK48288	Human bone marrow	C 305	21.8	0.4	79	20	AAK86611	PCR primer Orig1084
C 233	22.2	0.4	75	22	AAI26190	Probe #16123 for g	C 306	21.8	0.4	81	19	AAV32124	HLI9, antisense ch
C 234	22.2	0.4	75	22	AAI54113	Human genome-deriv	C 307	21.8	0.4	81	19	AAV32174	HLI9, antisense ch
C 235	22.2	0.4	75	22	ABS22150	DNA coding for the	C 308	21.8	0.4	82	21	AAAC20138	Human breast cell
C 236	22.2	0.4	83	22	AAZ99661	Human foetal liver	C 309	21.8	0.4	90	22	ABA50653	Human foetal liver
C 237	22.2	0.4	83	22	ABA70805	Probe #15750 for g	C 310	21.8	0.4	90	22	ABA55567	Human foetal liver
C 238	22.2	0.4	83	22	AAK19061	Human brain expres	C 311	21.8	0.4	90	22	AAK16550	Human brain expres
C 239	22.2	0.4	83	22	AAK45015	Human bone marrow	C 312	21.8	0.4	90	22	AAK42725	Human bone marrow
C 240	22.2	0.4	83	22	AAI25106	Probe #15039 for g	C 313	21.8	0.4	90	22	AAI23481	Probe #17484 used t
C 241	22.2	0.4	83	22	AAI25092	Probe #19668 used	C 314	21.8	0.4	90	22	AAI48798	Probe #9098 used t
C 242	22.2	0.4	83	22	ABSI9261	Human genome-deriv	C 315	21.8	0.4	90	22	AAI48798	Probe #9098 used t
C 243	22.2	0.4	83	22	ABSI9261	Human genome-deriv	C 316	21.8	0.4	90	22	AAI48798	Probe #9098 used t
C 244	22.2	0.4	83	22	AAI80696	Human pituitary CR	C 317	21.8	0.4	90	22	AAI48798	Probe #9098 used t
C 245	22.2	0.4	87	16	AAO81853	Human cell death p	C 318	21.8	0.4	90	22	AAI48798	Probe #9098 used t
C 246	22.2	0.4	87	16	AAO81853	Human cell death p	C 319	21.8	0.4	90	22	AAI48798	Probe #9098 used t
C 247	22.2	0.4	87	16	AAO81853	Human cell death p	C 320	21.8	0.4	90	22	AAI48798	Probe #9098 used t
C 248	22.2	0.4	94	24	ABSI77973	Coupled ligation a	C 321	21.8	0.4	91	13	AAV44955	Human nervous syst
C 249	22.2	0.4	94	24	ABSI77973	Coupled ligation a	C 322	21.8	0.4	91	13	AAV44955	Human nervous syst
C 250	22.2	0.4	94	24	ABSI77973	Coupled ligation a	C 323	21.8	0.4	91	13	AAV44955	Human nervous syst
C 251	22.2	0.4	97	21	AAI18621	Human secreted pro	C 324	21.8	0.4	92	13	AAO33827	Human IRG27 relate
C 252	22.2	0.4	97	21	AAI18621	Human secreted pro	C 325	21.8	0.4	92	13	AAO33827	Human IRG27 relate
C 253	22.2	0.4	99	22	AAH84217	Human cell death p	C 326	21.8	0.4	96	20	AAO33827	Human IRG27 relate
C 254	22.2	0.4	99	22	AAH84217	Human cell death p	C 327	21.8	0.4	96	20	AAO33827	Human IRG27 relate
C 255	22.2	0.4	99	22	AAH84217	Human cell death p	C 328	21.8	0.4	96	20	AAO33827	Human IRG27 relate
C 256	22.2	0.4	100	14	ABO60639	Yeast GCN4 variant	C 329	21.8	0.4	96	20	AAO33827	Human IRG27 relate
C 257	22.2	0.4	100	14	ABO60639	Yeast GCN4 variant	C 330	21.8	0.4	96	20	AAO33827	Human IRG27 relate
C 258	22.2	0.4	100	14	ABO60639	Yeast GCN4 variant	C 331	21.8	0.4	96	20	AAO33827	Human IRG27 relate
C 259	22.2	0.4	51	22	AAI27973	Fuzzy C3d gene tra	C 332	21.8	0.4	99	24	ABL60638	Yeast GCN4 variant
C 260	22.2	0.4	53	24	ABN20784	Streptococcus agal	C 333	21.8	0.4	99	24	ABL60638	Yeast GCN4 variant
C 261	22.2	0.4	58	16	AAI20784	Human gene signatu	C 334	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 262	22.2	0.4	64	24	AAI20784	Human gene signatu	C 335	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 263	22.2	0.4	64	24	AAI20784	Human gene signatu	C 336	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 264	22.2	0.4	65	24	AAI20784	Human gene signatu	C 337	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 265	22.2	0.4	65	24	AAI20784	Human gene signatu	C 338	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 266	22.2	0.4	65	24	AAI20784	Human gene signatu	C 339	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 267	22.2	0.4	65	24	AAI20784	Human gene signatu	C 340	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 268	22.2	0.4	65	24	AAI20784	Human gene signatu	C 341	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 269	22.2	0.4	65	24	AAI20784	Human gene signatu	C 342	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 270	22.2	0.4	65	24	AAI20784	Human gene signatu	C 343	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 271	22.2	0.4	65	24	AAI20784	Human gene signatu	C 344	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 272	22.2	0.4	65	24	AAI20784	Human gene signatu	C 345	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 273	22.2	0.4	65	24	AAI20784	Human gene signatu	C 346	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 274	22.2	0.4	65	24	AAI20784	Human gene signatu	C 347	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 275	22.2	0.4	65	24	AAI20784	Human gene signatu	C 348	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 276	22.2	0.4	65	24	AAI20784	Human gene signatu	C 349	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 277	22.2	0.4	65	24	AAI20784	Human gene signatu	C 350	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 278	22.2	0.4	65	24	AAI20784	Human gene signatu	C 351	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 279	22.2	0.4	65	24	AAI20784	Human gene signatu	C 352	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 280	22.2	0.4	65	24	AAI20784	Human gene signatu	C 353	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 281	22.2	0.4	65	24	AAI20784	Human gene signatu	C 354	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 282	22.2	0.4	65	24	AAI20784	Human gene signatu	C 355	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 283	22.2	0.4	65	24	AAI20784	Human gene signatu	C 356	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 284	22.2	0.4	65	24	AAI20784	Human gene signatu	C 357	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 285	22.2	0.4	65	24	AAI20784	Human gene signatu	C 358	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 286	22.2	0.4	65	24	AAI20784	Human gene signatu	C 359	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 287	22.2	0.4	65	24	AAI20784	Human gene signatu	C 360	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 288	22.2	0.4	65	24	AAI20784	Human gene signatu	C 361	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 289	22.2	0.4	65	24	AAI20784	Human gene signatu	C 362	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 290	22.2	0.4	65	24	AAI20784	Human gene signatu	C 363	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 291	22.2	0.4	65	24	AAI20784	Human gene signatu	C 364	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 292	22.2	0.4	65	24	AAI20784	Human gene signatu	C 365	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 293	22.2	0.4	65	24	AAI20784	Human gene signatu	C 366	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 294	22.2	0.4	65	24	AAI20784	Human gene signatu	C 367	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 295	22.2	0.4	65	24	AAI20784	Human gene signatu	C 368	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 296	22.2	0.4	65	24	AAI20784	Human gene signatu	C 369	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 297	22.2	0.4	65	24	AAI20784	Human gene signatu	C 370	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 298	22.2	0.4	65	24	AAI20784	Human gene signatu	C 371	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 299	22.2	0.4	65	24	AAI20784	Human gene signatu	C 372	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 300	22.2	0.4	65	24	AAI20784	Human gene signatu	C 373	21.8	0.4	100	22	AAAC65405	Human colon tumou
C 301	22.2	0.4	65	24	AAI20784	Human gene signatu	C 374	21.8	0.4	100	22	AAAC65405	Human colon tumou





667	20.8	0.4	76	22	AA109675	Probe #9666 used t	740	20.8	0.4	97	20	AAV99518	Synthetic lysine-r
668	20.8	0.4	79	14	AA048355	Mb 25D2 heavy cha	741	20.8	0.4	97	20	AAV99528	Synthetic lysine-r
669	20.8	0.4	79	16	AA098862	Anti-human IL-4 MA	742	20.8	0.4	98	20	AAV77393	Kawasaki disease a
670	20.8	0.4	80	12	AA014745	Probe jnh1-16 for	743	20.8	0.4	98	21	ABN80999	Shrimp polynucleot
671	20.8	0.4	80	14	AA046673	Ovine GHG primer o	744	20.8	0.4	98	22	AA065404	Oligonucleotide B6
672	20.8	0.4	80	19	AA014569	Human bisallelic po	745	20.8	0.4	99	15	AA065400	Cuphea hookeriana
673	20.8	0.4	80	22	AAH25157	Polynucleotide seq	746	20.8	0.4	99	19	AAV11608	Homo sapiens adult
674	20.8	0.4	81	17	AA188556	Secretory phosphol	747	20.8	0.4	99	21	AAH87288	Rat hepatocyte car
675	20.8	0.4	83	15	AA066926	Polyd detection p	748	20.8	0.4	99	21	AAA77789	Human foetal liver
676	20.8	0.4	83	22	AA523578	tetracycline promo	749	20.8	0.4	99	21	AAA36702	CDNA encoding huma
677	20.8	0.4	84	12	AA015231	BBP42 signal sequ	750	20.8	0.4	99	22	AAH72954	Muv and MV fusion
678	20.8	0.4	84	13	AA035822	Sequence upstream	751	20.8	0.4	99	22	AAK21385	Human brain expres
679	20.8	0.4	84	14	AA037283	Oligomer SM 96 use	752	20.8	0.4	99	22	AAK47546	Human bone marrow
680	20.8	0.4	84	14	AA037284	SSP(5)4 Oligonucle	753	20.8	0.4	99	22	AAI28527	Colon tumour relat
681	20.8	0.4	84	16	AA094998	SSP(5)4 Oligonucle	754	20.8	0.4	99	22	AAI53378	Human CDNA clone B
682	20.8	0.4	84	16	AA094999	Oligonucleotide SM	755	20.8	0.4	99	22	AAI53378	Human prostate exp
683	20.8	0.4	84	20	AAV99533	Bacillus lichenifo	756	20.8	0.4	99	23	ABV99084	Insertion sequence
684	20.8	0.4	84	24	ABK77100	Bacillus lichenifo	757	20.8	0.4	100	14	AA050291	Candida albicans-s
685	20.8	0.4	85	19	AAV32418	Homo sapiens clone	758	20.8	0.4	100	15	AA062589	Oligonucleotide B6
686	20.8	0.4	85	22	AAE98434	Human CDNA clone B	759	20.8	0.4	100	22	AA065405	Human genomic DNA
687	20.8	0.4	85	24	ABK77133	Bacillus lichenifo	760	20.8	0.4	31	21	AAV78905	Human genome biall
688	20.8	0.4	86	22	AA523317	Human prostate can	761	20.6	0.4	47	20	AAK52598	PCR primer used to
689	20.8	0.4	86	24	ABK77121	Bacillus lichenifo	762	20.6	0.4	49	21	AAK54009	PCR primer used to
690	20.8	0.4	86	24	ABK77134	Cat flea head and	763	20.6	0.4	49	21	AAK54010	Human silent SNP c
691	20.8	0.4	87	21	AA094368	HGF nucleic acid l	764	20.6	0.4	50	22	AAI79061	Human silent SNP c
692	20.8	0.4	87	22	AAE73659	Integrin alpha v b	765	20.6	0.4	51	22	AAI17148	Human SNP flanking
693	20.8	0.4	87	24	AAK31569	Human genome fragm	766	20.6	0.4	51	22	AAH39332	Human amino acid c
694	20.8	0.4	89	15	AA077525	Drosophila melanog	767	20.6	0.4	51	23	ABU009375	Oligonucleotide MF
695	20.8	0.4	89	15	AA077525	Human gene signatu	768	20.6	0.4	51	23	ABU009375	Nucleotide sequenc
696	20.8	0.4	89	22	AAH29032	HIV DNA encoding P	769	20.6	0.4	51	23	ABU009375	Mouse flt-1 VEGF r
697	20.8	0.4	90	16	AAI22382	Activated T-cell d	770	20.6	0.4	52	20	AAI16006	PCR primer C2-8 us
698	20.8	0.4	90	16	ABK36288	Human brain expres	771	20.6	0.4	52	20	AAI16006	Human spliced tran
699	20.8	0.4	90	24	ABK36381	Human brain expres	772	20.6	0.4	60	24	ABN32632	Human spliced tran
700	20.8	0.4	90	24	AAI69155	Human genome-deriv	773	20.6	0.4	60	24	ABN33039	Human spliced tran
701	20.8	0.4	91	16	AAI22379	Probe #17844 for g	774	20.6	0.4	60	24	ABN33039	Human spliced tran
702	20.8	0.4	91	16	AAI22379	Human bone marrow	775	20.6	0.4	60	24	ABN33039	Human spliced tran
703	20.8	0.4	91	22	AAI22558	Probe #16390 for g	776	20.6	0.4	60	24	ABN33039	Human spliced tran
704	20.8	0.4	91	22	AAI22558	Probe #16534 used	777	20.6	0.4	60	24	ABN33039	Human spliced tran
705	20.8	0.4	91	22	AAI22558	Human genome-deriv	778	20.6	0.4	60	24	ABN33039	Human spliced tran
706	20.8	0.4	92	16	AAI08517	Met-Arg-Met-platel	779	20.6	0.4	60	24	ABN33039	Human spliced tran
707	20.8	0.4	92	16	AAI08517	Human foetal liver	780	20.6	0.4	60	24	ABN33039	Human spliced tran
708	20.8	0.4	92	22	ABK39578	Probe #17844 for g	781	20.6	0.4	60	24	ABN33039	Human spliced tran
709	20.8	0.4	92	22	ABK39578	Human brain expres	782	20.6	0.4	60	24	ABN33039	Human spliced tran
710	20.8	0.4	92	22	AAK49227	Human bone marrow	783	20.6	0.4	60	24	ABN33039	Human spliced tran
711	20.8	0.4	92	22	AAK49227	Probe #23749 used	784	20.6	0.4	60	24	ABN33039	Human spliced tran
712	20.8	0.4	92	22	AAI26457	Human genome-deriv	785	20.6	0.4	60	24	ABN33039	Human spliced tran
713	20.8	0.4	92	22	AAI26457	Haemophilus alphaz	786	20.6	0.4	60	24	ABN33039	Human spliced tran
714	20.8	0.4	92	24	ABK02801	Human cervical can	787	20.6	0.4	60	24	ABN33039	Human spliced tran
715	20.8	0.4	93	22	AAH72107	Human secreted pro	788	20.6	0.4	60	24	ABN33039	Human spliced tran
716	20.8	0.4	94	21	AAI2575	Human breast cell	789	20.6	0.4	60	24	ABN33039	Human spliced tran
717	20.8	0.4	94	22	ABK50797	Human foetal liver	790	20.6	0.4	60	24	ABN33039	Human spliced tran
718	20.8	0.4	94	22	ABK50797	Probe #14192 for g	791	20.6	0.4	60	24	ABN33039	Human spliced tran
719	20.8	0.4	94	22	ABK50797	Human brain expres	792	20.6	0.4	60	24	ABN33039	Human spliced tran
720	20.8	0.4	94	22	ABK50797	Human brain expres	793	20.6	0.4	60	24	ABN33039	Human spliced tran
721	20.8	0.4	94	22	AAK4216	Human bone marrow	794	20.6	0.4	60	24	ABN33039	Human spliced tran
722	20.8	0.4	94	22	AAK4216	Probe #17652 used	795	20.6	0.4	60	24	ABN33039	Human spliced tran
723	20.8	0.4	94	22	AAI48966	Probe #24895 used	796	20.6	0.4	60	24	ABN33039	Human spliced tran
724	20.8	0.4	94	22	AAI48966	Probe #9262 used t	797	20.6	0.4	60	24	ABN33039	Human spliced tran
725	20.8	0.4	94	22	AAI56209	Humanised antibody	798	20.6	0.4	60	24	ABN33039	Human spliced tran
726	20.8	0.4	95	16	AA048076	Human gene signatu	799	20.6	0.4	60	24	ABN33039	Human spliced tran
727	20.8	0.4	95	16	AA048076	Human secreted pro	800	20.6	0.4	60	24	ABN33039	Human spliced tran
728	20.8	0.4	95	21	AAI26495	Shrimp polynucleot	801	20.6	0.4	60	24	ABN33039	Human spliced tran
729	20.8	0.4	96	21	AAI26495	Clone D16 used in	802	20.6	0.4	60	24	ABN33039	Human spliced tran
730	20.8	0.4	97	14	AA037270	SSP 5.5.5.5 clone	803	20.6	0.4	60	24	ABN33039	Human spliced tran
731	20.8	0.4	97	14	AA037270	SSP 5.5.5.5 clone	804	20.6	0.4	60	24	ABN33039	Human spliced tran
732	20.8	0.4	97	16	AA094993	SSP 5.5.5.5 clone	805	20.6	0.4	60	24	ABN33039	Human spliced tran
733	20.8	0.4	97	16	AA094993	SSP 5.5.5.5 clone	806	20.6	0.4	60	24	ABN33039	Human spliced tran
734	20.8	0.4	97	16	AA094993	SSP 5.5.5.5 clone	807	20.6	0.4	60	24	ABN33039	Human spliced tran
735	20.8	0.4	97	16	AA094993	SSP 5.5.5.5 clone	808	20.6	0.4	60	24	ABN33039	Human spliced tran
736	20.8	0.4	97	18	AA094993	Wheat germ aggluti	809	20.6	0.4	60	24	ABN33039	Human spliced tran
737	20.8	0.4	97	19	AAV35831	Synthetic storage	810	20.6	0.4	60	24	ABN33039	Human spliced tran
738	20.8	0.4	97	19	AAV35831	Synthetic storage	811	20.6	0.4	60	24	ABN33039	Human spliced tran
739	20.8	0.4	97	19	AAV35831	Synthetic storage	812	20.6	0.4	60	24	ABN33039	Human spliced tran
740	20.8	0.4	97	19	AAV35831	Synthetic storage	813	20.6	0.4	60	24	ABN33039	Human spliced tran
741	20.8	0.4	97	19	AAV35831	Synthetic storage	814	20.6	0.4	60	24	ABN33039	Human spliced tran
742	20.8	0.4	97	19	AAV35831	Synthetic storage	815	20.6	0.4	60	24	ABN33039	Human spliced tran
743	20.8	0.4	97	19	AAV35831	Synthetic storage	816	20.6	0.4	60	24	ABN33039	Human spliced tran
744	20.8	0.4	97	19	AAV35831	Synthetic storage	817	20.6	0.4	60	24	ABN33039	Human spliced tran
745	20.8	0.4	97	19	AAV35831	Synthetic storage	818	20.6	0.4	60	24	ABN33039	Human spliced tran
746	20.8	0.4	97	19	AAV35831	Synthetic storage	819	20.6	0.4	60	24	ABN33039	Human spliced tran
747	20.8	0.4	97	19	AAV35831	Synthetic storage	820	20.6	0.4	60	24	ABN33039	Human spliced tran
748	20.8	0.4	97	19	AAV35831	Synthetic storage	821	20.6	0.4	60	24	ABN33039	Human spliced tran
749	20.8	0.4	97	19	AAV35831	Synthetic storage	822	20.6	0.4	60	24	ABN33039	Human spliced tran
750	20.8	0.4	97	19	AAV35831	Synthetic storage	823	20.6	0.4	60	24	ABN33039	Human spliced tran
751	20.8	0.4	97	19	AAV35831	Synthetic storage	824	20.6	0.4	60	24	ABN33039	Human spliced tran
752	20.8	0.4	97	19	AAV35831	Synthetic storage	825	20.6	0.4	60	24	ABN33039	Human spliced tran
753	20.8	0.4	97	19	AAV35831	Synthetic storage	826	20.6	0.4	60	24	ABN33039	Human spliced tran
754	20.8	0.4	97	19	AAV35831	Synthetic storage	827	20.6	0.4	60	24	ABN33039	Human spliced tran
755	20.8	0.4	97	19	AAV35831	Synthetic storage	828	20.6	0.4	60	24	ABN33039	Human spliced tran
756	20.8	0.4	97	19	AAV35831	Synthetic storage	829	20.6	0.4	60	24	ABN33039	Human spliced tran
757	20.8	0.4	97	19	AAV35831	Synthetic storage	830	20.6	0.4	60	24	ABN33039	Human spliced tran
758	20.8	0.4	97	19	AAV35831	Synthetic storage	831	20.6	0.4	60	24	ABN33039	Human spliced tran
759	20.8	0.4	97	19	AAV35831	Synthetic storage	832	20.6	0.4	60	24	ABN33039	Human spliced tran
760	20.8	0.4	97	19	AAV35831	Synthetic storage	833	20.6	0.4	60	24	ABN33039	Human spliced tran
761	20.8	0.4	97	19	AAV35831	Synthetic storage	834	20.6	0.4	60	24	ABN33039	Human spliced tran
762	20.8	0.4	97	19	AAV35831	Synthetic storage	835	20.6	0.4	60	24	ABN33039	Human spliced tran
763	20.8	0.4	97	19	AAV35831	Synthetic storage	836	20.6	0.4	60	24	ABN3303	



813	20.6	0.4	77	21	AAC29105	Human secreted pro
814	20.6	0.4	77	21	AAZ29301	Sense primer for i
815	20.6	0.4	78	19	AAV62642	Humanized antibody
816	20.6	0.4	78	19	AAV32118	LH13 antisense ch
817	20.6	0.4	78	19	AAV32126	LH13 antisense hu
818	20.6	0.4	78	19	AAV32168	LH13 antisense ch
819	20.6	0.4	78	19	AAV32176	LH13 antisense hu
820	20.6	0.4	78	19	AAV32176	Oligonucleotide 4
821	20.6	0.4	80	20	AAV32805	Bacillus sp. GUS g
822	20.6	0.4	80	21	AAV9797	Secreted microb
823	20.6	0.4	81	16	AAV6222	HIV-1 reverse tran
824	20.6	0.4	81	18	AAV57930	L-selectin family
825	20.6	0.4	81	21	AAV37368	Primer CD-3-10 use
826	20.6	0.4	81	22	AAV43746	Cornedestrosin sin
827	20.6	0.4	82	22	AAV40731	Human brain expres
828	20.6	0.4	82	22	AAV42485	Human brain expres
829	20.6	0.4	82	22	AAV42485	Human bone marrow
830	20.6	0.4	82	24	AAV42485	Human genome-deriv
831	20.6	0.4	84	22	AAV42485	Human breast cell
832	20.6	0.4	84	22	AAV42485	Human foetal liver
833	20.6	0.4	84	22	AAV42485	Human foetal liver
834	20.6	0.4	84	22	AAV42485	Human brain expres
835	20.6	0.4	84	22	AAV42485	Human genome-deriv
836	20.6	0.4	84	22	AAV42485	Probe #14226 for g
837	20.6	0.4	84	22	AAV42485	Probe #18256 used
838	20.6	0.4	84	22	AAV42485	Human genome-deriv
839	20.6	0.4	84	22	AAV42485	VEGF nucleic acid
840	20.6	0.4	84	22	AAV42485	Human genome-deriv
841	20.6	0.4	84	22	AAV42485	Probe #15700 for g
842	20.6	0.4	84	22	AAV42485	Human bone marrow
843	20.6	0.4	84	22	AAV42485	Human bone marrow
844	20.6	0.4	84	22	AAV42485	Probe #15700 for g
845	20.6	0.4	84	22	AAV42485	Human genome-deriv
846	20.6	0.4	84	22	AAV42485	Human bone marrow
847	20.6	0.4	84	22	AAV42485	Human bone marrow
848	20.6	0.4	84	22	AAV42485	Probe #15700 for g
849	20.6	0.4	84	22	AAV42485	Human genome-deriv
850	20.6	0.4	84	22	AAV42485	Human bone marrow
851	20.6	0.4	84	22	AAV42485	Human bone marrow
852	20.6	0.4	84	22	AAV42485	Probe #15700 for g
853	20.6	0.4	84	22	AAV42485	Human genome-deriv
854	20.6	0.4	84	22	AAV42485	Human bone marrow
855	20.6	0.4	84	22	AAV42485	Human bone marrow
856	20.6	0.4	84	22	AAV42485	Probe #15700 for g
857	20.6	0.4	84	22	AAV42485	Human genome-deriv
858	20.6	0.4	84	22	AAV42485	Human bone marrow
859	20.6	0.4	84	22	AAV42485	Human bone marrow
860	20.6	0.4	84	22	AAV42485	Probe #15700 for g
861	20.6	0.4	84	22	AAV42485	Human genome-deriv
862	20.6	0.4	84	22	AAV42485	Human bone marrow
863	20.6	0.4	84	22	AAV42485	Human bone marrow
864	20.6	0.4	84	22	AAV42485	Probe #15700 for g
865	20.6	0.4	84	22	AAV42485	Human genome-deriv
866	20.6	0.4	84	22	AAV42485	Human bone marrow
867	20.6	0.4	84	22	AAV42485	Human bone marrow
868	20.6	0.4	84	22	AAV42485	Probe #15700 for g
869	20.6	0.4	84	22	AAV42485	Human genome-deriv
870	20.6	0.4	84	22	AAV42485	Human bone marrow
871	20.6	0.4	84	22	AAV42485	Human bone marrow
872	20.6	0.4	84	22	AAV42485	Probe #15700 for g
873	20.6	0.4	84	22	AAV42485	Human genome-deriv
874	20.6	0.4	84	22	AAV42485	Human bone marrow
875	20.6	0.4	84	22	AAV42485	Human bone marrow
876	20.6	0.4	84	22	AAV42485	Probe #15700 for g
877	20.6	0.4	84	22	AAV42485	Human genome-deriv
878	20.6	0.4	84	22	AAV42485	Human bone marrow
879	20.6	0.4	84	22	AAV42485	Human bone marrow
880	20.6	0.4	84	22	AAV42485	Probe #15700 for g
881	20.6	0.4	84	22	AAV42485	Human genome-deriv
882	20.6	0.4	84	22	AAV42485	Human bone marrow
883	20.6	0.4	84	22	AAV42485	Human bone marrow
884	20.6	0.4	84	22	AAV42485	Probe #15391 for g
885	20.6	0.4	84	22	AAV42485	Probe #20535 used
886	20.6	0.4	88	24	ABN20222	Human genome-deriv
887	20.4	0.4	100	24	ABN03162	Biotinylated inter
888	20.4	0.4	45	18	ABN03162	Class II MHC I-Ag7
889	20.4	0.4	45	21	ABN04053	Human map-related
890	20.4	0.4	47	21	AAZ69017	Human secreted pro
891	20.4	0.4	50	22	AAZ69017	Human SNP oligonuc
892	20.4	0.4	50	22	AAZ69017	Streptococcus agal
893	20.4	0.4	51	22	AAZ69017	Human silent SNP c
894	20.4	0.4	51	22	AAZ69017	Human silent SNP c
895	20.4	0.4	54	21	AAZ69017	Human secreted pro
896	20.4	0.4	54	21	AAZ69017	Human protective p
897	20.4	0.4	57	15	AAZ69017	Schistosoma manso
898	20.4	0.4	57	15	AAZ69017	Schistosoma manso
899	20.4	0.4	57	19	AAZ69017	Primer 7 for human
900	20.4	0.4	59	21	AAZ69017	Spacer DNA #2 from
901	20.4	0.4	59	21	AAZ69017	Trichoderma reesei
902	20.4	0.4	60	21	AAZ69017	Eucalyptus grandis
903	20.4	0.4	60	21	AAZ69017	PAPPL1-TfAFP gene
904	20.4	0.4	60	21	AAZ69017	RNA clone 21.08 fo
905	20.4	0.4	60	21	AAZ69017	Human spliced tran
906	20.4	0.4	60	21	AAZ69017	Human spliced tran
907	20.4	0.4	60	21	AAZ69017	Human spliced tran
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909	20.4	0.4	60	21	AAZ69017	Human spliced tran
910	20.4	0.4	60	21	AAZ69017	Human spliced tran
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915	20.4	0.4	60	21	AAZ69017	Human spliced tran
916	20.4	0.4	60	21	AAZ69017	Human spliced tran
917	20.4	0.4	60	21	AAZ69017	Human spliced tran
918	20.4	0.4	60	21	AAZ69017	Human spliced tran
919	20.4	0.4	60	21	AAZ69017	Human spliced tran
920	20.4	0.4	60	21	AAZ69017	Human spliced tran
921	20.4	0.4	60	21	AAZ69017	Human spliced tran
922	20.4	0.4	60	21	AAZ69017	Human spliced tran
923	20.4	0.4	60	21	AAZ69017	Human spliced tran
924	20.4	0.4	60	21	AAZ69017	Human spliced tran
925	20.4	0.4	60	21	AAZ69017	Human spliced tran
926	20.4	0.4	60	21	AAZ69017	Human spliced tran
927	20.4	0.4	60	21	AAZ69017	Human spliced tran
928	20.4	0.4	60	21	AAZ69017	Human spliced tran
929	20.4	0.4	60	21	AAZ69017	Human spliced tran
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934	20.4	0.4	60	21	AAZ69017	Human spliced tran
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937	20.4	0.4	60	21	AAZ69017	Human spliced tran
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940	20.4	0.4	60	21	AAZ69017	Human spliced tran
941	20.4	0.4	60	21	AAZ69017	Human spliced tran
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944	20.4	0.4	60	21	AAZ69017	Human spliced tran
945	20.4	0.4	60	21	AAZ69017	Human spliced tran
946	20.4	0.4	60	21	AAZ69017	Human spliced tran
947	20.4	0.4	60	21	AAZ69017	Human spliced tran
948	20.4	0.4	60	21	AAZ69017	Human spliced tran
949	20.4	0.4	60	21	AAZ69017	Human spliced tran
950	20.4	0.4	60	21	AAZ69017	Human spliced tran
951	20.4	0.4	60	21	AAZ69017	Human spliced tran
952	20.4	0.4	60	21	AAZ69017	Human spliced tran
953	20.4	0.4	60	21	AAZ69017	Human spliced tran
954	20.4	0.4	60	21	AAZ69017	Human spliced tran
955	20.4	0.4	60	21	AAZ69017	Human spliced tran
956	20.4	0.4	60	21	AAZ69017	Human spliced tran
957	20.4	0.4	60	21	AAZ69017	Human spliced tran
958	20.4	0.4	60	21	AAZ69017	Human spliced tran

RSV and HIV fusion	AAA36665	92	21
Oligonucleotide B6 <td>AAV65406 <td>92 <td>22</td> </td></td>	AAV65406 <td>92 <td>22</td> </td>	92 <td>22</td>	22
DNA sequence of pr <td>AAV61266 <td>93 <td>19</td> </td></td>	AAV61266 <td>93 <td>19</td> </td>	93 <td>19</td>	19
Prostate tumour sp <td>AAV58690 <td>93 <td>19</td> </td></td>	AAV58690 <td>93 <td>19</td> </td>	93 <td>19</td>	19
Human secreted pro <td>AAV30692 <td>93 <td>21</td> </td></td>	AAV30692 <td>93 <td>21</td> </td>	93 <td>21</td>	21
Human immunogenic <td>AAV06453 <td>93 <td>21</td> </td></td>	AAV06453 <td>93 <td>21</td> </td>	93 <td>21</td>	21
Human prostate CDN <td>AAV63661 <td>93 <td>22</td> </td></td>	AAV63661 <td>93 <td>22</td> </td>	93 <td>22</td>	22
Androgen responsiv <td>AAV15787 <td>93 <td>22</td> </td></td>	AAV15787 <td>93 <td>22</td> </td>	93 <td>22</td>	22
Human prostate tum <td>AAV10212 <td>93 <td>22</td> </td></td>	AAV10212 <td>93 <td>22</td> </td>	93 <td>22</td>	22
Human prostate-spe <td>AAV93569 <td>93 <td>22</td> </td></td>	AAV93569 <td>93 <td>22</td> </td>	93 <td>22</td>	22
Prostate tumour spe <td>AAV84883 <td>93 <td>22</td> </td></td>	AAV84883 <td>93 <td>22</td> </td>	93 <td>22</td>	22
Human 8-hillev cdn <td>AAV02634 <td>93 <td>22</td> </td></td>	AAV02634 <td>93 <td>22</td> </td>	93 <td>22</td>	22
Oligonucleotide B6 <td>AAV69749 <td>93 <td>24</td> </td></td>	AAV69749 <td>93 <td>24</td> </td>	93 <td>24</td>	24
Human secreted pro <td>AAV65407 <td>93 <td>24</td> </td></td>	AAV65407 <td>93 <td>24</td> </td>	93 <td>24</td>	24
Human secreted pro <td>AAV19442 <td>95 <td>21</td> </td></td>	AAV19442 <td>95 <td>21</td> </td>	95 <td>21</td>	21
Human secreted pro <td>AAV25786 <td>95 <td>22</td> </td></td>	AAV25786 <td>95 <td>22</td> </td>	95 <td>22</td>	22
Human bone marrow <td>AAV43726 <td>96 <td>13</td> </td></td>	AAV43726 <td>96 <td>13</td> </td>	96 <td>13</td>	13
Encodes His(177) m <td>AAV20799 <td>96 <td>13</td> </td></td>	AAV20799 <td>96 <td>13</td> </td>	96 <td>13</td>	13
Encodes Ala(182) m <td>AAV20802 <td>96 <td>13</td> </td></td>	AAV20802 <td>96 <td>13</td> </td>	96 <td>13</td>	13
Polyclonal anti-fe <td>AAV70233 <td>96 <td>18</td> </td></td>	AAV70233 <td>96 <td>18</td> </td>	96 <td>18</td>	18
Human foetal liver <td>AAV71184 <td>96 <td>22</td> </td></td>	AAV71184 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Probe #15428 for 9 <td>AAV36962 <td>96 <td>22</td> </td></td>	AAV36962 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Human brain expres <td>AAV37512 <td>96 <td>22</td> </td></td>	AAV37512 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Human brain expres <td>AAV18459 <td>96 <td>22</td> </td></td>	AAV18459 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Human bone marrow <td>AAV19481 <td>96 <td>22</td> </td></td>	AAV19481 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Human bone marrow <td>AAV44364 <td>96 <td>22</td> </td></td>	AAV44364 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Probe #14771 for 9 <td>AAV5473 <td>96 <td>22</td> </td></td>	AAV5473 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Probe #15216 for 9 <td>AAV24838 <td>96 <td>22</td> </td></td>	AAV24838 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Probe #19049 used <td>AAV50363 <td>96 <td>22</td> </td></td>	AAV50363 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Human genome-deriv <td>AAV15148 <td>96 <td>22</td> </td></td>	AAV15148 <td>96 <td>22</td> </td>	96 <td>22</td>	22
Human genome-deriv <td>ABV18600 <td>96 <td>24</td> </td></td>	ABV18600 <td>96 <td>24</td> </td>	96 <td>24</td>	24
Synthetic plant pr <td>ABV19740 <td>97 <td>24</td> </td></td>	ABV19740 <td>97 <td>24</td> </td>	97 <td>24</td>	24
Human gene express <td>ABV2087 <td>98 <td>20</td> </td></td>	ABV2087 <td>98 <td>20</td> </td>	98 <td>20</td>	20
Human secreted pro <td>AAV14151 <td>98 <td>20</td> </td></td>	AAV14151 <td>98 <td>20</td> </td>	98 <td>20</td>	20
Human secreted pro <td>AAV14676 <td>99 <td>21</td> </td></td>	AAV14676 <td>99 <td>21</td> </td>	99 <td>21</td>	21
Human breast cell <td>AAV14807 <td>99 <td>21</td> </td></td>	AAV14807 <td>99 <td>21</td> </td>	99 <td>21</td>	21
Human foetal liver <td>ABV7289 <td>100 <td>22</td> </td></td>	ABV7289 <td>100 <td>22</td> </td>	100 <td>22</td>	22
	ABV65174 <td>100 <td>22</td> </td>	100 <td>22</td>	22

## ALIGNMENTS

## RESULT 1

ABN35465 standard; DNA: 60 BP.

15-JUL-2002 (first entry)

Human spliced transcript detection oligonucleotide SEQ ID NO:8213.

Human; mouse; rat; splice transcript; detection; RNA transcript;

splice variant; transcriptome; oligonucleotide library; ss.

Homo sapiens.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-1B01903.

28-JUL-2000; 2000US-221607P.

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides which  
selectively hybridize to mRNAs transcribed from a transcription unit of  
a genome, useful for detecting tissue-, pathology-, and  
developmental-specific genes.

Example 1; SEQ ID 8213; 47pp; English.

The present invention describes oligonucleotide libraries for detecting  
messenger RNAs that populate a (sub-)transcriptome, where the  
(sub-)transcriptome comprises messenger RNAs transcribed from multiple  
transcription units that populate a genome. The library comprises  
several oligonucleotides, each capable of hybridizing selectively to a  
set of messenger RNAs transcribed from a given transcription unit of  
the genome, which encodes one or more messenger RNA splice variants.  
The oligonucleotide libraries are useful for detecting mRNAs from a  
biological sample. In expression profiling studies, in qualitatively or  
quantitatively characterizing the corresponding transcriptome, and in  
detecting RNA transcripts and splice variants of human or animal  
transcriptomes. The libraries may also be used as human or animal  
libraries to detect transcripts of a sub-transcriptome under a  
particular biological or pathological state, and so allowing the  
detection of tissue- and pathology-specific genes such as those genes  
only expressed in specific tissue under a specific pathological  
condition; to detect developmental specific genes; and to detect RNA  
transcripts and splice variants of a transcriptome of a patient suffering  
from a particular disorder. ABN27253 to ABN59589 represent  
CC oligonucleotide sequences from rats, humans and mice, which are used in  
CC N.B. The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from WIP0  
at ftp.wipo.int/pub/published\_pcl\_sequences.

Sequence 60 BP; 17 A; 17 C; 10 G; 16 T; 0 other;

Query Match 1.2%; Score 60; DB 24; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4560 ATAGCCCTTTTAACTGCAAGACTGACAGCTGACAGCTGACAGCTGCTCTCT 4619  
Db 1 ATAGCCCTTTTAACTGCAAGACTGACAGCTGACAGCTGACAGCTGCTCTCTCT 60

## RESULT 2

ABN55582/C standard; DNA: 65 BP.

15-JUL-2002 (first entry)

Mouse spliced transcript detection oligonucleotide SEQ ID NO:28330.

Human; mouse; rat; splice transcript; detection; RNA transcript;

splice variant; transcriptome; oligonucleotide library; ss.

Mus musculus.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-1B01903.

28-JUL-2000; 2000US-221607P.

02-MAY-2001; 2001US-287724P.

(COMP-) COMPUGEN INC.



The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also useful in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

The present invention relates to antisense compounds, compositions and methods for modulating the expression of MEK4 (also referred as mitogen activated protein kinase kinase 4; MAP3K4, MAP three kinase 1; MAP3ERK kinase 4; MAPKK4; MTK1). The antisense oligos are useful for inhibiting the expression of MEK4 in cells or tissues. They are also useful for treating an animal having a disease or condition associated with MEK4 such as immunological, inflammatory, hyperproliferative disorder or cancer. Sequences of the invention are also useful for diagnostics, therapeutics, prophylaxis and as research reagents and kits. They are also useful in antisense therapy. The present sequence is a PCR probe which is used for amplifying human MEK4 DNA. This sequence



```

PR 12-MAR-1999;      99DE-1011044.
PA (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
XX Karl J., Lill H., Stahl P., Krueger K., Borgia A., Gallusser A.;
DR WPI; 2000-499359/44.
XX
PT Identification of N-terminal pro-brain natriuretic peptide (pro-BNP)
PT using two antibodies that recognize different epitopes of the
PT N-terminal pro-BNP, useful for diagnosis of heart insufficiency -
XX
PS Example 1; Page 32; 35pp; German.
CC
CC This invention describes a novel method to detect N-terminal pro-brain
CC natriuretic peptide (BNP) in a sample using two antibodies, that
CC recognize different epitopes of the N-terminal pro-BNP. The method can
CC be used for diagnosing heart insufficiency. The recombinant N-terminal
CC pro-BNP is useful as a standard in a method to detect N-terminal pro-BNP
CC and also for production of antibodies against N-terminal pro-BNP.
CC This sequence represents a primer used in the cloning of recombinant
CC N-terminal proBNP which is described in the method of the invention.
SO Sequence 70 BP; 10 A; 19 C; 21 G; 20 T; 0 other;
Query Match          0.5%; Score 25.2; DB 21; Length 70;
Best Local Similarity 62.9%; Pred.No. 4.9e+03;
Matches   39; Conservative    0; Mismatches   23; Indels     0; Gaps     0;
OY 1778 AGGGGCGCTGTGATGAAGCAGTACTACGATTTCCTGCAGGAGTTCTGGAGCACT 1837
DB ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
  8 AGGGGCGCTGTGTAACCTGCAGTGCGAGTTTACCCTGCAGGTGGTACGCTGTCC 67
OY 1838 TG 1839
DB ||
  68 TG 69
RESULT 11
AAT22086
ID AAT22086 standard; cDNA to mRNA; 89 BP.
XX AC
XX AAT22086;
DT 02-AUG-1996 (first entry)
XX DE
XX Human gene signature HUMS03631.
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW human; cloning; mapping; non-biased library; diagnosis; detection;
KW cell typing; abnormal cell function; ss.
XX OS
XX Homo sapiens.
XX PN
XX NC09514772-Al.
XX PD
XX 01-JUN-1995.
XX PF
XX 11-NOV-1994; 94MO-JP01916.
XX PR
XX 12-NOV-1993; 93JP-0355504.
XX PA
XX (MATS/) MATSUBARA K.
XX PA (OKUBO/) OKUBO K.
XX PI Matsubara K., Okubo K.;
XX DR
XX WPI; 1995-206931/27.
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function, by preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues

```

XX PS Claim 1; Page 1039; 2245bp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 GS sequences  
 CC given in AAT19001-726837 and which is able to hybridize to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridize with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.

XX Sequence 89 BP; 39 A; 8 C; 15 G; 27 T; 0 other;

SO Query Match 0.5%; Score 25.2; DB 16; Length 89;  
 CC Best Local Similarity 62.9%; Pred. No. 5.8e+03;  
 CC Matches 39; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 4485 AGAATATGACCTTGGAATTCCTTAATCACTACTGATGTAATTTACATTAAGACT 4544  
 DB 13 ACAAAAGTTTCATGGAATATATTAAATAGTACGTTTATGTCTTAATTAAGACT 72

OY 4545 GT 4546  
 DB 73 GT 74

RESULT 12  
 ID AAT92244 standard; DNA; 99 BP.  
 XX AAT92244;  
 AC AAT92244;  
 AT 19-JAN-1998 (first entry)  
 DE Mercuric ion reductase mera PCR mutagenesis primer 307-339S.  
 XX Metal ion resistance; mercuric ion reductase; mera; mercury;  
 KW toxic heavy metal; transgenic plant; mutagenic; bacterial;  
 KW transposon; Tn21; PCR; ss.  
 XX Synthetic.  
 OS Transposon Tn21.  
 XX US5668294-A.  
 PN 16-SEP-1997.  
 PD 21-APR-1995; 95US-0427097.  
 PF 21-APR-1995; 95US-0427097.  
 PR (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA Meagher RB, Summers AO;  
 PI WPI: 1997-470112/43.  
 XX DNA encoding mercuric ion reductase in plant-expressible form - for  
 PT producing transgenic plants resistant to toxic heavy metals  
 PS Example 1; Column 43-44; 52pp; English.

CC The present sequence represents a PCR mutagenesis primer used to  
 CC mutagenise the mera coding sequence derived from transposon Tn21, to  
 CC adapt it for plant expressibility. The nucleic acid molecule produced

CC is useful for producing transgenic plants that are resistant to toxic  
 CC heavy metals (especially mercury) and so can be used remediate and/or  
 CC revegetate contaminated areas. The bacterial mera gene is derived from  
 CC the transposon Tn21, which was originally isolated from the  
 CC incompatibility Group IncFII resistance plasmid NRI.

SO Sequence 99 BP; 29 A; 21 C; 25 G; 24 T; 0 other;

XX Query Match 0.5%; Score 25.2; DB 18; Length 99;  
 CC Best Local Similarity 54.3%; Pred. No. 6.2e+03;  
 CC Matches 51; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 3026 ATGCTGACCTAATGCTGAGGTAGGATCAAGACCCAGTGGCGCATCAAGAT 3085  
 DB 2 AAGACCGACTATAGGTGAGCTGATCTGCTGCTTTCGATGGAAGCATTAAGTGC 61

OY 3086 TTGATTTTCTACAGCAATTTGAACCTGCTTAT 3119  
 DB 62 GTGAGCATCTACAGCAAGCAAGTTGCTTAT 95

RESULT 13  
 ID AA228594 standard; DNA; 99 BP.  
 XX AA228594;  
 AC AA228594;  
 AT 24-DEC-1999 (first entry)  
 DE Primer 307-339S for Tn21 mera gene.  
 XX Organometal; resistance; transcription; translation; regulation; mera;  
 KW transposon; Tn21; mera; mercuric ion reductase; organomercury lyase; ss;  
 KW transgenic plant; detoxification; metal compound; soil; sediment; primer;  
 KW aquatic environment; bioremediation; contamination; PCR; amplification.

XX Synthetic.  
 OS Transposon Tn21.  
 XX US5965796-A.  
 PN 12-OCT-1999.  
 PD 19-JUN-1997; 97US-0878957.  
 PF 21-APR-1995; 95US-0427097.  
 PR (UYGE-) UNIV GEORGIA RES FOUND INC.  
 PA Rugh CL, Meagher RB, Summers AO;  
 PI WPI: 1999-579950/49.  
 XX Metal resistance sequences for producing transgenic plants -  
 PS Example 3; Column 17-18; 71pp; English.

CC The invention relates to a nucleic acid molecule comprising a coding  
 CC sequence for an organometal resistance protein, which is operably  
 CC linked downstream of and under the regulatory control of a  
 CC plant-expressible transcription and translation regulatory sequence.  
 CC The organometal resistance gene is especially the mera gene from the  
 CC transposon Tn21 or the B-coli mera gene. mera encodes a mercuric ion  
 CC reductase and mera encodes a organomercury lyase. The nucleic acid  
 CC sequences are useful for producing transgenic plants which are capable  
 CC of efficiently processing mercury. These plants are able to remove or  
 CC detoxify metal compounds such as methyl mercury and ionic mercury from  
 CC soil, sediment, and aquatic environments providing an efficient  
 CC bioremediation of metal and organometal contaminated sites.  
 CC This sequence represents a PCR primer used to amplify the Tn21 mera  
 CC gene which is mutated by random mutagenesis (see AA228584-228589 for  
 CC mutated sequences) and the mutated sequences are expressed in the  
 CC transgenic plants of the invention.







KW human PIV1; HPIV2; HPIV3; RSV; pathogen; measles; PCR primer;  
 KW respiratory syncytial virus; respiratory tract infection; bovine; ss.  
 XX  
 OS Human respiratory syncytial virus.  
 XX  
 XX WO200142445-A2.  
 XX  
 XX 14-JUN-2001.  
 XX  
 XX 08-DEC-2000; 2000MO-US33293.  
 XX  
 XX 10-DEC-1999; 990S-0170195.  
 XX  
 XX 10-DEC-1999; 990S-0458813.  
 XX  
 XX 10-DEC-1999; 990S-0459062.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Murphy BR, Collins PL, Schmidt AC, Durbin AP, Skladopoulos MH;  
 PI Tao T;  
 XX  
 XX WPI; 2001-356173/37.  
 XX  
 XX Isolated infectious chimeric parainfluenza virus (PIV), useful in an  
 PT attenuated vaccine to elicits an immune response against one or more  
 PT virus(es) selected from human PIV1 (HPIV1), HPIV2 and HPIV3 -  
 XX  
 XX Example 10; Page 150; 305pp; English.  
 XX  
 XX The present sequence for reverse PCR primer for respiratory syncytial  
 CC virus (RSV) A G gene insert is used with the forward PCR primer  
 CC (AA506929) in the construction of bovine/humanPIV3-RSV chimeric viruses.  
 CC The sequence is described in an invention relating to novel infectious  
 CC chimeric parainfluenza viruses (PIVs). The virus comprises a major  
 CC nucleocapsid protein (N), a nucleocapsid phosphoprotein (P), a large  
 CC polymerase protein (L), and a partial or complete PIV vector backbone  
 CC genome, or antigenome combined with one or more heterologous gene(s) or  
 CC more heterologous pathogen(s) to form a chimeric genome or antigenome.  
 CC The chimeric PIV is useful in an attenuated vaccine to elicit an immune  
 CC response against one or more virus(es) selected from human PIV1 (HPIV1),  
 CC HPIV2 and HPIV3. The chimeric PIV may also elicit a polyclonal immune  
 CC response against HPIV3, measles or RSV. An immunospecific composition  
 CC may also contain two chimeric PIVs, where the first chimeric PIV elicits  
 CC an immune response against HPIV3 and the second chimeric PIV elicits an  
 CC immune response against HPIV1 or HPIV2, and where both the first and  
 CC second chimeric PIVs elicit an immune response against the non-PIV  
 CC pathogen. Chimeric HPIV3, HPIV1 and HPIV2 are useful as vaccines to  
 CC prevent measles and upper or lower respiratory tract infections  
 CC particularly in young children.  
 CC  
 XX Sequence 92 BP; 20 A; 12 C; 26 G; 34 T; 0 other;  
 XX  
 XX Query Match 0.5%; Score 24.8; DB 22; Length 92;  
 XX Best Local Similarity 63.3%; Pred. No. 7.7e+03;  
 XX Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;  
 XX  
 QY 45 TACCTCCCTCCCGACGACGACCTGACAGATGAACGATGTCACCAACATCAGAGAA 104  
 DB 80 TTATCTCCACGACGACGACGACGACGATGTAAGTAAGTAAGTAAGTAAGTAAGTA 21  
 XX  
 XX RESULT 19  
 XX AAC11499  
 XX ID AAC11499 standard; cDNA; 94 BP.  
 XX  
 XX AAC11499;  
 XX  
 XX 06-OCT-2000 (first entry)  
 XX  
 XX Human secreted protein 5' EST, SEQ ID NO: 15574.  
 XX  
 XX Human, 5' EST, expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.

XX  
 OS Homo sapiens.  
 XX  
 XX EP1033401-A2.  
 XX  
 XX 06-SEP-2000.  
 XX  
 XX 21-FEB-2000; 2000EP-0200610.  
 XX  
 XX 26-FEB-1999; 990S-0122487.  
 XX  
 XX (GSEST ) GENSET.  
 XX  
 XX Dumas Milne Edwards J, Duclert A, Giordano J;  
 DR WPI; 2000-500361/45.  
 XX  
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 XX Claim 1; SEQ ID 15574; 71pp + CD-ROM; English.  
 XX  
 XX The present sequence is one of a large number of 5' ESTs derived from  
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively  
 CC identified within the present sequence. The 5' ESTs were prepared from  
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST  
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)  
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA  
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences  
 CC derived from the 5' ends of mRNAs and even in those cases where longer  
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.  
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be  
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used  
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 CC They are used to obtain upstream regulatory sequences and to design  
 CC expression and secretion vectors.  
 CC  
 XX Sequence 94 BP; 46 A; 9 C; 14 G; 25 T; 0 other;  
 XX  
 XX Query Match 0.5%; Score 24.8; DB 21; Length 94;  
 XX Best Local Similarity 54.3%; Pred. No. 7.9e+03;  
 XX Matches 50; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 XX  
 QY 1379 GACCATTTGTAGACAAACGACGATGGGTTAGAAAGTTAATTTAAGACTTC 1438  
 DB 2 GAAATATATAAAATACATACCAAAAGAGTCGTAGCTAATGTAATTAATTAAGCTCC 61  
 XX  
 QY 1439 ACAAGCTAATGATGCTTCTTCCCAAGGGCA 1470  
 DB 62 AAGATTTAATGTAGCAAAATATTAATTAAGGCA 93  
 XX  
 XX RESULT 20  
 XX AAC15541/c  
 XX ID AAC15541 standard; cDNA; 94 BP.  
 XX  
 XX AAC15541;  
 XX  
 XX 06-OCT-2000 (first entry)  
 XX  
 XX Human secreted protein 5' EST, SEQ ID NO: 19616.  
 XX  
 XX Human, 5' EST, expressed sequence tag; secreted protein; cDNA isolation;  
 KW gene therapy; chromosome mapping; ss.  
 XX  
 XX Homo sapiens.  
 XX  
 XX EP1033401-A2.  
 XX  
 XX 06-SEP-2000.  
 XX  
 XX 21-FEB-2000; 2000EP-0200610.



PR 05-JUN-1995; 95US-0465594.  
 PR 07-JUN-1995; 95US-0479725.  
 PR 07-JUN-1995; 95US-0479783.  
 XX  
 PA (NEXS-) NEXSTAR PHARM INC.  
 XX  
 PI Gold L, Janjic N, Pagratlis N, Ringquist S, Toothman PJ;  
 DR WPI: 1997-034387/03.  
 XX  
 PT Identification of nucleic acid ligands to TGF-beta, PDGF and hKGF  
 PT using SELEX, used in the diagnosis and treatment of proliferative  
 XX disorders  
 PS  
 PS Claim 15; Page 123; 209pp; English.  
 XX  
 CC The present sequence, a transforming growth factor beta-1  
 CC (TGF-beta-1) binding ligand, was identified by Systematic Evolution  
 CC of Ligands by Exponential enrichment (SELEX). Briefly, a candidate  
 CC mixture of nucleic acids was contacted with TGF-beta-1, and nucleic  
 CC acids having an increased affinity to TGF-beta-1 partitioned from  
 CC the remainder of the mixture. The partitioned nucleic acids were  
 CC then amplified to yield a mixture of nucleic acids enriched for  
 CC sequences with higher affinity and specificity for binding to  
 CC TGF-beta-1. The ligand is anti-mitogenic and may be used to inhibit  
 CC epithelial cell proliferation, or in the diagnosis and treatment of  
 CC TGF-beta-1 mediated pathological conditions, e.g. fibrotic  
 CC conditions such as fibroids of the kidney, lung and liver and more  
 CC acute conditions such as dermal scarring and restenosis.  
 XX  
 SQ Sequence 71 BP; 15 A; 16 C; 22 G; 18 T; 0 other;  
 XX  
 Query Match 0.5%; Score 24.6; DB 18; Length 71;  
 Best Local Similarity 65.5%; Pred. No. 7.5e+03;  
 Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;  
 XX  
 QY 3958 GAACATGATGATGCTGATTCACAAAGCATCACCATTGGCATGACGCTCC 4012  
 Db 56 GAAGACGTAGTAGTAGTAGTAGTAGTAACATACATCCCTGCGCATGCTCTCC 2  
 XX  
 RESULT 23  
 ID AAA52344 standard; cDNA; 72 BP.  
 AC AAA52344;  
 XX  
 DT 18-SEP-2000 (first entry)  
 XX  
 DE cDNA encoding Drosophila Doubletime (DBT) ATP binding domain.  
 XX  
 KW ATP binding domain; Doubletime; DBT; casein kinase family protein;  
 KW serine/threonine kinase; Period; PER; phosphorylation; stability;  
 KW circadian rhythm; clock; sleep disorder; depression; narcolepsy;  
 KW jet lag; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 US6057129-A.  
 PN  
 XX  
 PD 02-MAY-2000.  
 XX  
 PF 19-JUN-1998; 98US-0100664.  
 XX  
 PR 19-JUN-1998; 98US-0100664.  
 XX  
 PA (UVRQ) UNITV ROCKEFELLER.  
 XX  
 PI Young MW, Blau J, Price J, Kloss B;  
 XX WPI: 2000-338602/29.  
 DR P-PSDB; AAB01926.  
 XX

PT Novel nucleic acids encoding clock protein, doubletime which is useful  
 PT for treating disorders of circadian rhythm such as jet lag and mental  
 XX disorders  
 XX  
 PS Claim 25; Column 71-72; 61pp; English.  
 XX  
 CC This sequence represents cDNA encoding the ATP binding domain of the  
 CC Drosophila circadian rhythm protein Doubletime (DBT). DBT (AAB01923) is  
 CC a member of the casein kinase protein family and comprises an ATP  
 CC binding domain (AAB01926) and a serine/threonine kinase catalytic domain  
 CC (AAB01927). It plays a role in regulating the concentration of the clock  
 CC protein Period (PER). PER acts together with Timeless (TIM) in the  
 CC mediation of the circadian rhythm. The PER protein is normally unstable  
 CC in the cytoplasm, but is stabilised on heterodimerisation with TIM. The  
 CC PER/TIM heterodimer translocates to the nucleus where it regulates the  
 CC transcription of the per and tim genes through a negative feedback loop.  
 CC Because PER/TIM heterodimers are only present in large numbers when high  
 CC levels of per and tim RNA have accumulated, self-sustained oscillations  
 CC are produced in the negative feedback loop. DBT plays a key role in the  
 CC destabilisation of cytoplasmic PER monomers. It phosphorylates PER at  
 CC several sites, with a high level of PER phosphorylation correlating  
 CC with increased instability and degradation. The invention also  
 CC discloses two mutant DBT proteins, DBT-S and DBT-L (AAB01924 and  
 CC AAB01925, respectively). The DBT-S protein is associated with a  
 CC shortened (faster) circadian rhythm, while the DBT-L protein is  
 CC associated with a lengthened (slower) circadian rhythm. The DBT-S mutant  
 CC appears to phosphorylate PER more rapidly than the wild-type protein,  
 CC resulting in the premature degradation of monomeric PER. While the action  
 CC of DBT-L causes hypophosphorylation and persistence of monomeric PER in  
 CC the cytoplasm. DBT mutants, nucleotides encoding them, DBT agonists  
 CC and antagonists may be used in the prevention and/or treatment of  
 CC circadian rhythm disorders including depression, narcolepsy, jet lag, and  
 CC other sleep-wake cycle mental disorders.  
 XX  
 SQ Sequence 72 BP; 18 A; 19 C; 23 G; 12 T; 0 other;  
 XX  
 Query Match 0.5%; Score 24.6; DB 21; Length 72;  
 Best Local Similarity 59.2%; Pred. No. 7.5e+03;  
 Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
 XX  
 QY 3694 ATTGAGAGAGCGCATTATGGGAGAGGTGTACCTGCATCAGCGTGCAGCGGAGCTG 3753  
 Db 1 ATAGGATCGGAGTCGTTCGGCGACATCTACCTGGGCACACGATCACTGGCGAGAG 60  
 XX  
 QY 3754 ATGGCCATGAA 3764  
 Db 61 GTGGCCATCAA 71  
 XX  
 RESULT 24  
 ID ABR36568 standard; DNA; 90 BP.  
 AC ABR36568;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE HCV DNA encoding HepC1a segment 133.  
 XX  
 KW Saving; vaccine; cancer; viral infection; HIV; hepatitis C virus;  
 KW viral infection; human immunodeficiency virus; melanoma;  
 KW bacterial infection; Salmonella; Legionella; parasitic infection;  
 KW Trypanosoma; Toxoplasma; Giardia; ds.  
 XX  
 OS Hepatitis C virus.  
 XX  
 WO200190197-A1.  
 PN  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 25-MAY-2001; 2001MO-AU00622.  
 XX  
 PR 26-MAY-2000; 2000AU-0007761.  
 XX

XX (AUSU ) UNIV AUSTRALIAN NAT.  
 PA Thomson SA, Ramshaw IA;  
 XX  
 XX WPI: 2002-147575/19.  
 DR P-PSDB; AAU84730.  
 XX  
 XX New synthetic polypeptides having several different segments of at  
 PT least one parent polypeptide linked together differently compared to  
 PT the linkage in the parent polypeptide, for inducing immune response  
 PT against a pathogen or cancer  
 PS  
 XX Example 2; Fig 26; 364pp; English.  
 XX  
 XX The invention relates to a new synthetic polypeptide (I) comprising  
 CC several different segments of at least one parent polypeptide linked  
 CC together in a different relationship relative to their linkage in the  
 CC parent polypeptide to impede, abrogate or otherwise alter at least one  
 CC function associated with the parent polypeptide and for inducing an  
 CC immune response against a pathogen or cancer. Also included are a  
 CC synthetic polynucleotide encoding and a computer system for  
 CC designing the synthetic polypeptides. The synthetic polypeptides and  
 CC polynucleotides are referred to as a vaccine. The synthetic polypeptide is  
 CC useful for modulating immune responses preferably directed against a  
 CC pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix,  
 CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone  
 CC liver, oesophagus, brain, testicle, uterus), as potentiating agents, or  
 CC compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present  
 CC sequence encodes a peptide derived from a parent protein used to  
 CC construct a vaccine of the invention.  
 XX  
 SQ Sequence 90 BP; 22 A; 23 C; 21 G; 24 T; 0 other;  
 Query Match 0.5%; Score 24.6; DB 24; Length 90;  
 Best Local Similarity 59.2%; Pred. No. 8.8e+03;  
 Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
 QY 2274 CCGGAAATAGCAGAGATTTCAGGCCAGTTCAGAGACCTCGATGTTCT 2333  
 DB 80 CCAGGCGATTGGGCGATTCAGTTGGCTTCAGCCAGGTTTGAATCGCTGAGCATTGG 21  
 QY 2334 GAATCAAAAC 2344  
 DB 20 CAATCAATC 10  
 RESULT 25  
 AAX23469/c  
 ID AAX23469 standard; DNA; 98 BP.  
 AC AAX23469;  
 XX  
 DT 17-JUN-1999 (first entry)  
 XX  
 DE Human neutrophil cDNA clone 876.  
 XX  
 XX Neutrophil: gene expression profile; granulocyte; pathogen-exposed;  
 KW sterile inflammatory disease; detection; therapeutic agent; human;  
 KW expression modulator; pathogenic infection; cell activation; primer;  
 KW global transcriptional response; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9910536-A1.  
 XX

PD 04-MAR-1999.  
 XX  
 XX 21-AUG-1998; 98WO-US17284.  
 XX  
 XX 22-AUG-1997; 97US-0056844.  
 XX  
 XX (UYVA ) UNIV YALE.  
 PA  
 PI Goguen J, Newburger P, Prashar Y, Weissman SM, Yerramilli SV;  
 XX WPI: 1999-204678/17.  
 DR  
 XX  
 XX Detection of pathogen exposure or sterile inflammatory disease in a  
 PT subject - by comparing gene expression profiles from granulocytes  
 PT of the patient and control granulocytes  
 PS  
 XX Example 3; Page 41; 84pp; English.  
 XX  
 XX This invention describes a method for the comparison of gene expression  
 CC profiles from granulocytes from a test subject and from pathogen exposed  
 CC or sterile inflammatory disease granulocytes or quiescent granulocytes.  
 CC The method is used to detect pathogen exposure or sterile inflammatory  
 CC disease in a subject and to identify therapeutic agents that modulate  
 CC expression of a gene in response to a pathogenic infection or to  
 CC sterile inflammatory disease in a subject. The method tests for global  
 CC transcriptional response of granulocytes during cell activation.  
 XX  
 SQ Sequence 98 BP; 30 A; 16 C; 20 G; 32 T; 0 other;  
 Query Match 0.5%; Score 24.6; DB 20; Length 98;  
 Best Local Similarity 59.2%; Pred. No. 9.3e+03;  
 Matches 42; Conservative 0; Mismatches 29; Indels 0; Gaps 0;  
 QY 4911 GTTCTATTCGAAAGGCGTGAATTCGAAATTAAGAAAGGTTCTTTTCATTAAT 4970  
 DB 93 GTTATCATACATAGACCGCATCTATATACAAAGGGGGTTCTTTTTCATTAAAC 34  
 QY 4971 GGTATTATTTA 4981  
 DB 33 GTTACAAATATA 23  
 RESULT 26  
 AAX25128  
 ID AAX25128 standard; DNA; 82 BP.  
 AC AAX25128;  
 XX  
 DT 05-JUL-1999 (first entry)  
 XX  
 DE 80% Bundle peptide-encoding oligonucleotide.  
 XX  
 KW Flavivirus; dengue virus; envelope protein; vaccine; infection;  
 KW diagnosis; ds.  
 XX  
 OS Synthetic.  
 XX  
 FH key Location/Qualifiers  
 FT misc-feature 82  
 FT /tag= "a  
 FT /note= "Single stranded overhang on complementary  
 FT strand of sequence 5'-TCCA-3'  
 FT  
 XX  
 XX WO9906068-A2.  
 XX  
 XX 11-FEB-1999.  
 PD  
 XX 27-JUL-1998; 98WO-US15447.  
 PF  
 XX 31-JUL-1997; 97US-0904227.  
 PR  
 XX  
 PA (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.  
 XX

PI Coller BG, Harada KE, Ivy JM, McDonnell M, Peters ID;  
XX WPI: 1999-153454/13.  
XX Recombinant dimeric flaviviral envelope vaccine - comprising a  
PT dimeric 80kE protein, useful for protecting against flavivirus,  
PT especially dengue virus infections  
XX  
PS Example 4; Page 30; 60pp; English.  
XX  
CC This double-stranded oligonucleotide was annealed to another  
CC double-stranded oligonucleotide (see AAX25127) to generate a DNA  
CC sequence encoding the C-terminal half of a linker and  
CC helix-turn-helix domain (see AAY05526). This was utilized in the  
CC construction of an expression vector for secretion of  
CC non-covalently linked 80kE Bundle, where 80kE comprises a  
CC C-terminally truncated envelope (E) protein (see AAY05522) of  
CC dengue virus serotype 2 strain PR159/SI, and Bundle is the linker  
CC and helix-turn-helix moiety that is designed to form a  
CC non-covalently associated 4-helix bundle domain that enhances the  
CC dimerisation of the 80kE molecule. A vaccine for protecting  
CC against DEN-2 infection comprises a dimeric 80kE protein that has  
CC been secreted as a recombinant protein from a eukaryotic cell.  
XX  
SQ Sequence 82 BP; 19 A; 19 C; 32 G; 12 T; 0 other;  
XX  
Query Match 0.5%; Score 24.4; DB 20; Length 82;  
Best Local Similarity 63.8%; Pred. No. 9.4e+03;  
Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
XX  
QY 1789 CTGATGAGGAGTACTACAGTTCATGTCGACAGGAGTCTGTGGAGACCTGGAGAGC 1846  
DB 1 CTGCTGAGAGGCCCCCGCAAGGCGAGCTGGAGAGCTGCTGAAGACCTGAAGAGC 58  
XX  
RESULT 27  
ABA68615/C  
ID ABA68615 standard; DNA; 99 BP.  
XX  
AC ABA68615;  
XX  
DT 01-FEB-2002 (first entry)  
XX  
DE Human foetal liver single exon nucleic acid probe #16920.  
XX  
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200157277-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00669.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
PS WPI: 2001-483447/52.  
XX  
PT Human genome-derived single exon nucleic acid probes useful for  
PT analyzing gene expression in human fetal liver  
XX  
PS Claim 4; SEQ ID NO 16920; 639bp + sequence listing; English.

XX  
CC The invention relates to a single exon nucleic acid probe for  
CC measuring human gene expression in a sample derived from human foetal  
CC liver. The single exon nucleic acid probes may be used for predicting,  
CC measuring and displaying gene expression in samples derived from human  
CC fetal liver. The present sequence is a single exon nucleic acid  
CC probe of the invention.  
CC Note: The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 99 BP; 25 A; 14 C; 35 G; 25 T; 0 other;  
XX  
Query Match 0.5%; Score 24.4; DB 22; Length 99;  
Best Local Similarity 58.1%; Pred. No. 1.1e+04;  
Matches 43; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
XX  
QY 751 AATGTAATGTCGATGAGAGGCGATGCAAGCCACTGCTGGACAAAGATTGAGTTAC 810  
DB 94 AATGTAATGTCGATGAGAGGCGATGCAAGCCACTGCTGGACCAATGATGATCTCTC 35  
XX  
QY 811 TCAACACATCATGA 824  
DB 34 TGACCTCATCATCA 21  
XX  
RESULT 28  
ABA35588/C  
ID ABA35588 standard; DNA; 99 BP.  
XX  
AC ABA35588;  
XX  
DT 23-JAN-2002 (first entry)  
XX  
DE Probe #14054 for gene expression analysis in human heart cell sample.  
XX  
KW Human; gene expression; heart; microarray; vascular system; probe;  
KW cardiovascular disease; hypertension; cardiac arrhythmia;  
KW congenital heart disease; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200157274-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 30-JAN-2001; 2001WO-US00666.  
XX  
PR 04-FEB-2000; 2000US-0180312.  
PR 26-MAY-2000; 2000US-0207456.  
PR 30-JUN-2000; 2000US-0608408.  
PR 03-AUG-2000; 2000US-0632366.  
PR 21-SEP-2000; 2000US-0234687.  
PR 27-SEP-2000; 2000US-0236359.  
PR 04-OCT-2000; 2000GB-0024263.  
XX  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
XX  
PI Penn SG, Hanzel DK, Chen W, Rank DR;  
XX  
PS WPI: 2001-488899/53.  
XX  
PT Single exon nucleic acid probes for analyzing gene expression in human  
PT hearts -  
XX  
PS Claim 4; SEQ ID NO 14054; 530pp; English.  
XX  
CC The present invention relates to single exon nucleic acid probes for  
CC measuring human gene expression in a sample derived from human heart. The  
CC present sequence is one such probe. The probes may be used for  
CC predicting, measuring and displaying gene expression in samples derived  
CC from the human heart via microarrays. By measuring gene expression, the  
CC probes are useful for predicting, diagnosing, grading, staging,



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ID      AAK21231 standard; DNA; 80 BP.
XX
AC      AAK21231;
XX
DT      05-NOV-2001 (first entry)
XX
DE      Human brain expressed single exon probe SEQ ID NO: 21222.
XX
KW      Human; brain expressed exon; gene expression analysis; probe;
KW      microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW      epilepsy; cancer; ss.
XX
OS      Homo sapiens.
XX
MO      200157275-A2.
XX
PD      09-AUG-2001.
XX
PF      30-JAN-2001; 2001WO-US00667.
XX
PR      04-FEB-2000; 2000US-0180312.
PR      26-MAY-2000; 2000US-0207456.
PR      30-JUN-2000; 2000US-0608408.
PR      03-AUG-2000; 2000US-0632366.
PR      21-SEP-2000; 2000US-0234687.
PR      27-SEP-2000; 2000US-0236359.
PR      04-OCT-2000; 2000GB-0024263.
XX
PA      (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI      Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WI      WPI; 2001-483446/52.
XX
PT      Single exon nucleic acid probes for analyzing gene expression in human
XX      brains -
XX
PS      Example 4; SEQ ID NO: 21222; 650bp + Sequence listing; English.
XX
CC      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      brain. They can be used to measure gene expression in brain cell samples,
CC      which may enable the diagnosis and improved treatment of nervous system
CC      diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC      epilepsy and cancers. The present sequence is one of the probes of the
CC      invention.
XX
SQ      Sequence 80 BP; 18 A; 15 C; 13 G; 34 T; 0 other;
XX
Query Match      0.5%; Score 24.2; DB 22; Length 80;
Best Local Similarity 62.3%; Pred. No. 1.1e+04;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0
OY      3462 AAGAAAGACTTGGGAACCTTCGACACTAATCAATCCAGCACTAAAGATACGCTTTAAACT 3521
DB      66 AAGAAATTATCAAGCACTGTGACATTTAAGGCCACAGAAATCATCTGTTATAAATT 7
OY      3522 A 3522
DB      6 A 6
RESULT 32
AAK47388/C
ID      AAK47388 standard; DNA; 80 BP.
XX
AC      AAK47388;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human bone marrow expressed single exon probe SEQ ID NO: 21945.
XX
KW      Human; bone marrow expressed exon; gene expression analysis; probe;
XX

```

XX	microarray; cancer; leukemia; lymphoma; myeloma; ss.
OS	Homo sapiens.
XX	WO200157276-A2.
PN	09-AUG-2001.
XX	
PD	30-JAN-2001; 2001WO-US000668.
XX	
PF	04-FEB-2000; 2000US-0180312.
XX	26-MAY-2000; 2000US-0207456.
PR	30-JUN-2000; 2000US-0608408.
PR	03-AUG-2000; 2000US-0632366.
PR	21-SEP-2000; 2000US-0234687.
PR	27-SEP-2000; 2000US-0236359.
PR	04-OCT-2000; 2000GB-0024265.
XX	
PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;
DR	WPI; 2001-488900/53.
XX	
PT	Human genome-derived single exon nucleic acid probes useful for
PT	analyzing gene expression in human bone marrow -
XX	
PS	Example 4; SEQ ID NO: 21945; 658bp + Sequence Listing; English.
XX	
CC	The present invention provides a number of single exon nucleic acid
CC	probes which are derived from genomic sequences expressed in the human
CC	bone marrow. They can be used to measure gene expression in bone marrow
CC	samples, which may enable the improved diagnosis and treatment of cancers
CC	such as lymphoma, leukemia and myeloma. The present sequence is one of
XX	the probes of the invention.
XX	
SQ	Sequence 80 BP; 18 A; 15 C; 13 G; 34 T; 0 other;
XX	
Query Match	0.58; Score 24.2; DB 22; Length 80;
Best Local Similarity	62.3%; Pred. No. 1.1e+04;
Matches 38; Conservative	0; Mismatches 23; Indels 0; Gaps 0
QY	3462 AAGAAGAAGTTGGGAACTTGGAGACTATTCAGCCAGGTAAGTACTGTTCTAACT 3521
DB	66 AAGAAATTATTCACAGCACTGTGCACATTTTAAGGCCACGAAATCATCTCTGTTATTAATT 7
QY	3522 A 3522
DB	6 A 6
XX	
RESULT 33	
AAI53226/C	
ID	AAI53226 standard; DNA; 80 BP.
XX	
AC	AAI53226;
XX	
DT	17-OCT-2001 (first entry)
XX	
DE	Probe #21912 used to measure gene expression in human placenta sample.
XX	
KW	Probe; microarray; human; placenta; antenatal diagnosis;
KW	genetic disorder; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200157272-A2.
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US000663.
XX	
XX	04-FEB-2000; 2000US-0180312.





CC Compositions comprising the polypeptide may be used in the treatment or  
 CC prophylaxis against viral (such as infections caused by HIV (human  
 CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis  
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial  
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,  
 CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic  
 CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,  
 CC Trypanosoma, Toxoplasma and Giardia) infections. The present  
 CC sequence encodes a peptide derived from a parent protein used to  
 CC construct a vaccine of the invention.

SO Sequence 90 BP; 29 A; 19 C; 15 G; 19 T; 8 other;

Query Match  
 Best Local Similarity 55.6%; Score 24.2; DB 24; Length 90;  
 Matches 35; Conservative 5; Mismatches 23; Indels 0; Gaps 0;

OY 4100 GTTCGTAAGCTCAAAACATGCCAGCATGCTGCTGTAAGTACAGCAGCCCTGG 4159  
 DB 23 GGTCCGAGATTCACARACATGTCATTAATGCTCCATCCTCAACRAAGCCTCG 82  
 OY 4160 GGA 4162  
 DB 83 WGA 85

RESULT 36  
 AAH51645  
 ID AAH51645 standard; DNA; 94 BP.

AC AAH51645;

DT 29-AUG-2001 (first entry)

DE Sbg1 exon sequence SEQ ID 57.

XX Sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33; haplotype;  
 XX bi-allelic marker; polymorphism; schizophrenia; bipolar disorder; ds.

XX Pan troglodytes.

XX WO200058510-A2.

XX 05-OCT-2000.

PF 30-MAR-2000; 2000WO-IB00435.

PR 30-MAR-1999; 99US-0126903.

PR 30-APR-1999; 99US-0131971.

PR 14-JUL-1999; 99US-0132065.

PR 27-JUL-1999; 99US-0143928.

PR 29-JUL-1999; 99US-0145915.

PR 29-JUL-1999; 99US-0146452.

PR 28-OCT-1999; 99US-0146453.

XX 28-OCT-1999; 99US-0162288.

XX (GEST ) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I, Bougueleret L, Blahin B;

DR WPI; 2000-619082/59.

PT Polynucleotides comprising sequences from sbg1 and g35018 bi-allelic  
 PT markers are used for genotyping and detecting schizophrenia or bipolar  
 disorder and predisposition to these disorders.

PS Claim 1; Page 563; 737Pp; English.

CC AAH51601 represents a human genomic nucleotide sequence comprising sbg1,  
 CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the  
 CC human chromosome 13q31-q33 locus. The nucleotide sequences contain  
 CC bi-allelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and

CC AAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein  
 CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018  
 CC cDNA sequences and protein products. Primers AAH51632 - AAH51639 are used  
 CC to isolate sbg1 cDNAs, while sbg1 exons from different primates are  
 CC represented by sequences AAH51642 - AAH51699. Nucleotide sequences of  
 CC amplicons which comprise bi-allelic markers located on the chromosome  
 CC 13q31-q33 locus are represented in AAH51700 - AAH51817. Bi-allelic markers  
 CC are represented in the sequences by degenerate/undefined base codes. PCR  
 CC primers AAH51818 and AAH51819 are used in the isolation of sequences of  
 CC the invention. The bi-allelic marker containing nucleotide sequences are  
 CC used to determine the identity of the nucleotide at a bi-allelic marker in  
 CC a sample DNA sequence. The nucleotide sequences may be labelled and used  
 CC for genotyping by determining the identity of a nucleotide at a region  
 CC D-related bi-allelic marker in a biological sample from single or multiple  
 CC subjects. By determining the frequency of a bi-allelic marker in a  
 CC population an association between a genotype and a trait, a haplotype of  
 CC a trait and a phenotype and a trait can be detected. The sequences of  
 CC used to determine a predisposition to or early onset of schizophrenia or  
 CC bipolar disorder or a beneficial response to or side effects related to  
 CC treatment against schizophrenia or bipolar disorder.

SO Sequence 94 BP; 29 A; 15 C; 20 G; 30 T; 0 other;

Query Match  
 Best Local Similarity 78.4%; Score 24.2; DB 21; Length 94;  
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1048 AGCAATTATGACATTCGCTGCGCAGTGTTCGAA 1084  
 DB 46 AAGATTTCACATATTTCTGGCATTATGGA 82

RESULT 37

AAH51668  
 ID AAH51668 standard; DNA; 94 BP.

AC AAH51668;

DT 29-AUG-2001 (first entry)

DE Sbg1 exon sequence SEQ ID 80.

XX Sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33; haplotype;  
 XX bi-allelic marker; polymorphism; schizophrenia; bipolar disorder; ds.

XX Gorilla gorilla.

XX WO200058510-A2.

XX 05-OCT-2000.

PF 30-MAR-2000; 2000WO-IB00435.

PR 30-MAR-1999; 99US-0126903.

PR 30-APR-1999; 99US-0131971.

PR 14-JUL-1999; 99US-0132065.

PR 27-JUL-1999; 99US-0143928.

PR 29-JUL-1999; 99US-0145915.

PR 29-JUL-1999; 99US-0146452.

PR 28-OCT-1999; 99US-0162288.

XX (GEST ) GENSET.

PI Cohen D, Blumenfeld M, Chumakov I, Bougueleret L, Blahin B;

DR WPI; 2000-619082/59.

PT Polynucleotides comprising sequences from sbg1 and g35018 bi-allelic  
 PT markers are used for genotyping and detecting schizophrenia or bipolar  
 disorder and predisposition to these disorders.

PS Claim 1: Page 568; 737pp; English.

XX AAH51601 represents a human genomic nucleotide sequence comprising sbg1,  
 CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the  
 CC human chromosome 13q31-q33 locus. The nucleotide sequences contain  
 CC bi-allelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and  
 CC AAB62907 - AAB62915 represent cDNA sequences and protein  
 CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018  
 CC cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used  
 CC to isolate sbg1 cDNAs, while sbg1 exons from different primates are  
 CC represented by sequences bi-allelic markers located on the chromosome  
 CC 13q31-q33 locus are represented in AAH51700 - AAH51817. Bi-allelic markers  
 CC are represented in the sequences by degenerate/undefined base codes. PCR  
 CC primers AAH51818 and AAH51819 are used in the isolation of sequences of  
 CC the invention. The bi-allelic marker containing nucleotide sequences are  
 CC used to determine the identity of the nucleotide at a bi-allelic marker in  
 CC a sample DNA sequence. The nucleotide sequences may be labelled and used  
 CC for genotyping by determining the frequency of a nucleotide at a Region  
 CC D-related bi-allelic marker in a biological sample from single or multiple  
 CC subjects. By determining the frequency of a bi-allelic marker in a  
 CC population an association between a genotype and a trait, a haplotype and  
 CC a trait and an association between a genotype and a trait can be detected. The sequences can be  
 CC used to determine a predisposition to or early onset of schizophrenia or  
 CC bipolar disorder or a beneficial response to or side effects related to  
 CC treatment against schizophrenia or bipolar disorder.

XX Sequence 94 BP; 29 A; 15 C; 20 G; 30 T; 0 other;

SO Query Match 0.5%; Score 24.2; DB 21; Length 94;  
 Best Local Similarity 78.4%; Pred. No. 1.2e+04;  
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1048 AAGAAATTTTCAGATATTTGCTGGCGCACTTATGGA 1084  
 DB 46 AAGAAATTTTCAGATATTTGCTGGCGCACTTATGGA 82

RESULT 38  
 AAH51692 standard; DNA; 94 BP.

XX AAH51692:  
 AC 29-AUG-2001 (first entry)  
 DT Sbg1 exon sequence SEQ ID 104.  
 DE sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33; haplotype;  
 XX bi-allelic marker; polymorphism; schizophrenia; bipolar disorder; ds.  
 KW Macaca mulatta.  
 OS WO200058510-A2.  
 PN 05-OCT-2000.  
 PD 30-MAR-2000; 2000WO-IB00435.  
 PE 30-MAR-1999; 99US-0126993.  
 PR 30-APR-1999; 99US-0131971.  
 PR 30-APR-1999; 99US-0132065.  
 PR 1-JUL-1999; 99US-0143928.  
 PR 1-JUL-1999; 99US-0145915.  
 PR 2-JUL-1999; 99US-0146452.  
 PR 23-JUL-1999; 99US-0146453.  
 PR 28-OCT-1999; 99US-0162288.  
 PA (GEST) GENSET.  
 XX Cohen D, Blumenfeld M, Chumakov I, Bougueneloret L, Bihain B;  
 PI Essieux L;

DR WPI; 2000-619082/59.

XX Polynucleotides comprising sequences from sbg1 and g35018 bi-allelic  
 PT markers are used for genotyping and detecting schizophrenia or bipolar  
 CC disorder and predisposition to these disorders.

XX Claim 1: Page 573; 737pp; English.

XX AAH51601 represents a human genomic nucleotide sequence comprising sbg1,  
 CC g34665, sbg2, g35017 and g35018 nucleic acid sequences located on the  
 CC human chromosome 13q31-q33 locus. The nucleotide sequences contain  
 CC bi-allelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and  
 CC AAB62907 - AAB62915 represent cDNA sequences and protein  
 CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent g35018  
 CC cDNA sequences and protein products. Primers AAH51632 - AAH51699 are used  
 CC to isolate sbg1 cDNAs, while sbg1 exons from different primates are  
 CC represented by sequences bi-allelic markers located on the chromosome  
 CC 13q31-q33 locus are represented in AAH51700 - AAH51817. Bi-allelic markers  
 CC are represented in the sequences by degenerate/undefined base codes. PCR  
 CC primers AAH51818 and AAH51819 are used in the isolation of sequences of  
 CC the invention. The bi-allelic marker containing nucleotide sequences are  
 CC used to determine the identity of the nucleotide at a bi-allelic marker in  
 CC a sample DNA sequence. The nucleotide sequences may be labelled and used  
 CC for genotyping by determining the frequency of a nucleotide at a Region  
 CC D-related bi-allelic marker in a biological sample from single or multiple  
 CC subjects. By determining the frequency of a bi-allelic marker in a  
 CC population an association between a genotype and a trait, a haplotype and  
 CC a trait and an association between a genotype and a trait can be detected. The sequences can be  
 CC used to determine a predisposition to or early onset of schizophrenia or  
 CC bipolar disorder or a beneficial response to or side effects related to  
 CC treatment against schizophrenia or bipolar disorder.

XX Sequence 94 BP; 28 A; 16 C; 20 G; 30 T; 0 other;

SO Query Match 0.5%; Score 24.2; DB 21; Length 94;  
 Best Local Similarity 78.4%; Pred. No. 1.2e+04;  
 Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1048 AAGAAATTTTCAGATATTTGCTGGCGCACTTATGGA 1084  
 DB 46 AAGAAATTTTCAGATATTTGCTGGCGCACTTATGGA 82

RESULT 39  
 ABA71915/C  
 ID ABA71915 standard; DNA; 95 BP.

XX ABA71915:  
 AC 01-FEB-2002 (first entry)  
 DT Human foetal liver single exon nucleic acid probe #20220.  
 DE Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
 KW Homo sapiens.  
 OS WO200157277-A2.  
 PN 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US00669.  
 PE 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0609366.  
 PR 03-AUG-2000; 2000US-0634687.  
 PR 21-SEP-2000; 2000US-0236355.  
 PR 27-SEP-2000; 2000US-0236355.  
 PR 04-OCT-2000; 2000US-0024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483447/52.  
 DR  
 XX

PT Human genome-derived single exon nucleic acid probes useful for  
 XX analyzing gene expression in human fetal liver -  
 PS

XX Claim 4; SEQ ID NO 20220; 639pp + sequence listing; English.  
 CC

CC The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC fetal liver. The present sequence is a single exon nucleic acid  
 CC probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pcl\_sequences.  
 CC

SQ Sequence 95 BP; 21 A; 28 C; 13 G; 33 T; 0 other;  
 Query Match

Best Local Similarity 0.5%; Score 24.2; DB 22; Length 95;  
 Matches 41; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1142 AAGGAGATTAAAGGAGTTGGAAGTACGATGAGAGTGAAGAACAATCTCTG 1201  
 DB 88 ACGGAGAGTAATGGAATTAAGACTGACAGCAGACGCTGATTATGAAGAATGTCTC 29

QY 1202 ATCCTAGGG 1210  
 DB 28 AGGCTAAGG 20

# RESULT 40

AAK20302/c  
 ID AAK20302 standard; DNA; 95 BP.

XX AAK20302;  
 AC  
 XX

DN 05-NOV-2001 (first entry)  
 XX

DE Human brain expressed single exon probe SEQ ID NO: 20293.  
 XX

KW Human: brain expressed exon; gene expression analysis; probe;  
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 KW epilepsy; cancer; SS.  
 XX

OS Homo sapiens.  
 XX

PN WO200157275-A2.  
 XX

PD 09-AUG-2001.  
 XX

PF 30-JAN-2001; 2001WO-US00667.  
 XX

PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483446/52.  
 DR  
 XX

PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains -

XX Example 4; SEQ ID NO: 20293; 650pp + Sequence Listing; English.  
 PS  
 XX

CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention.  
 CC

SQ Sequence 95 BP; 21 A; 28 C; 13 G; 33 T; 0 other;  
 Query Match

Best Local Similarity 0.5%; Score 24.2; DB 22; Length 95;  
 Matches 41; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 1142 AAGGAGATTAAAGGAGTTGGAAGTACGATGAGAGTGAAGAACAATCTCTG 1201  
 DB 88 ACGGAGAGTAATGGAATTAAGACTGACAGCAGACGCTGATTATGAAGAATGTCTC 29

QY 1202 ATCCTAGGG 1210  
 DB 28 AGGCTAAGG 20

Search completed: November 11, 2002, 07:16:44  
 Job time: 660 secs